

	MS-GPC- 8-27-7	MS-GPC- 8-27-10	MS-GPC- 8-6-13	MS-GPC- 8-27-41	MS-GPC- 8-6-47	MS-GPC- 8-10-57	MS-GPC- 8-6-27	MS-GPC- 8	MS-GPC- 8-6
Plastic	-0.004	-0.020	-0.022	-0.025	-0.001	0.005	0.007	-0.022	-0.018
BSA	-0.003	-0.019	-0.021	-0.022	0.008	0.003	0.003	-0.016	-0.019
Testosterone -BSA	-0.005	-0.010	-0.012	-0.007	0.011	0.003	0.002	-0.009	-0.012
Lysozyme human	-0.005	-0.079	-0.079	-0.073	0.013	0.014	0.006	-0.081	-0.072
Apotransferrin	-0.009	-0.016	-0.018	-0.018	-0.005	-0.008	-0.004	-0.014	-0.016
MHCII (DRA*0101/ DRB1*0401)	1.549	1.493	1.467	1.525	1.400	1.256	1.297	1.058	1.306

Fig. 1A



100001934 .071602

#5

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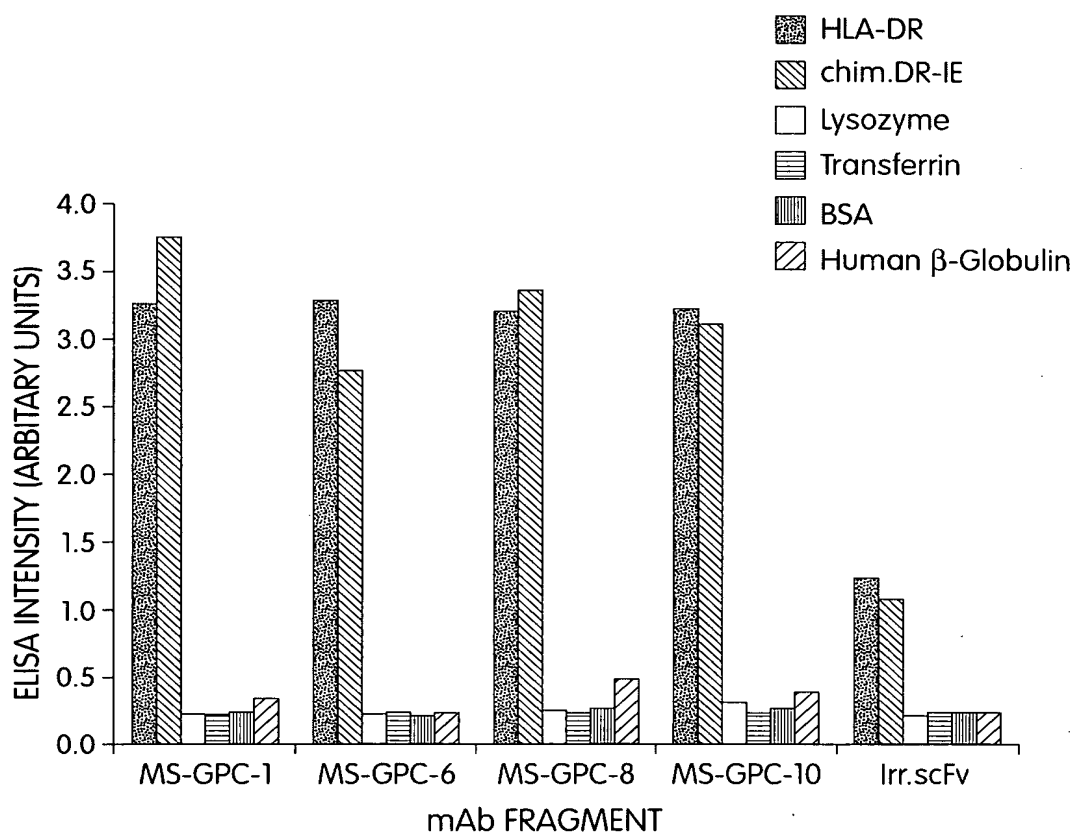


Fig. 1B

Target Proteins	scFv												IgG		
	17	2E	45	5C	73	8A	A1	B8	E6	FD	159	170	1D09C3	1C7277	305D3
DR4Dw4 Purified	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Chimeric DR-IE purified	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
Lysozyme	b	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Transferrin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BSA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Human gamma globulin	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

a. In Elisa, OD (at 370 nm - background): > 1.5

b. In Elisa, OD (at 370 nm - background): < 0.5

Fig. 1C

Cell Line	HLA-	DRB1*	scFv													IgG		
			17	2E	45	5C	73	8A	A1	B8	E6	FD	159	170	1D09C3	1C7277	305D3	
LG2	DR1	0101	+	+	b	-	+	+	+	+	+	+	+	+	+	+	+	
E4181324	DR2	15021	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+	
VAVY	DR3	0301	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+	
PRIESS	DR4Dw4	0401	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+/- <sup>c</sup>	
TS10	DR4Dw10	0402	+	+	-	+/-	+	+	+	+	+	+	+	+	+	+	+	
BIN40	DR4Dw14	0404	+	+	+	+/-	+	+	+	+	+	+	+	+	+	+	+	
TAB089	DR8	8031	+	+	-	+/-	+	+	+	+	+	+	+	+	+	+	+	
DKB	DR9	9012	+	+	+/-	+/-	+	+	+	+	+	+	+	+	+	+	+/-	
WT47	DR13	1302	+	+	-	-	+	+	+	+	+	+	+	+	+	+	+	
TEM	DR14	1401	+	+	+	+/-	+	+	+	+	+	+	+	+	+	+	+	
L105.1	DRw52	B3*0101	+	-	-	-	nt <sup>d</sup>	+	-	+	+	+	nt	nt	+/-	+/-	+/-	
L257.6	DRw53	B4*0101	+/-	-	+	-	nt	+	-	+	+/-	+/-	nt	nt	+	+	+	
L25.4	DPw4/w4.2	DP0103/0402	-	-	-	-	nt	+	-	-	-	-	nt	nt	+/-	-	+/-	
L256.12	DPw2/w2.1	DP0202/0201	-	-	-	-	nt	+/-	-	-	-	-	nt	nt	-	-	-	
L21.3	DQ7/w2	DQ0201/0602	-	-	-	-	nt	+	-	+	-	-	nt	nt	nt	nt	nt	
Target Cell			% Cells Killed <sup>e</sup>															
PRIESS			75	20	28	32	22	89	33	59	75	34	1	5	88	93	74	

a. FACS analysis, mAb + FITC-anti human IgG<sub>4</sub>, mean fluorescence intensity > 30.

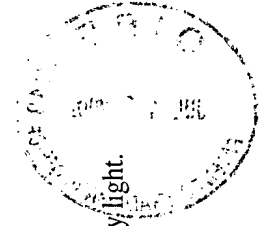
b. Mean fluorescence intensity < 10.

c. Mean fluorescence intensity 10-30.

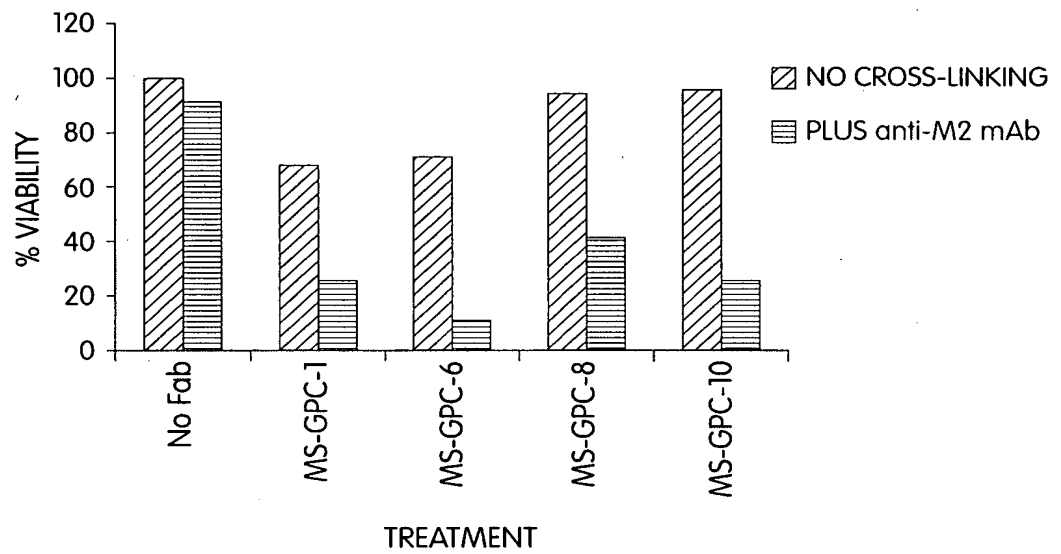
d. Not tested.

e. Based on viable cell recovery after treatment with 200nM scFv plus 100 nM anti-FLAG or 50 nM mab at 37°C for 4h. Determined by light.

Fig. 2



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**Fig. 3**

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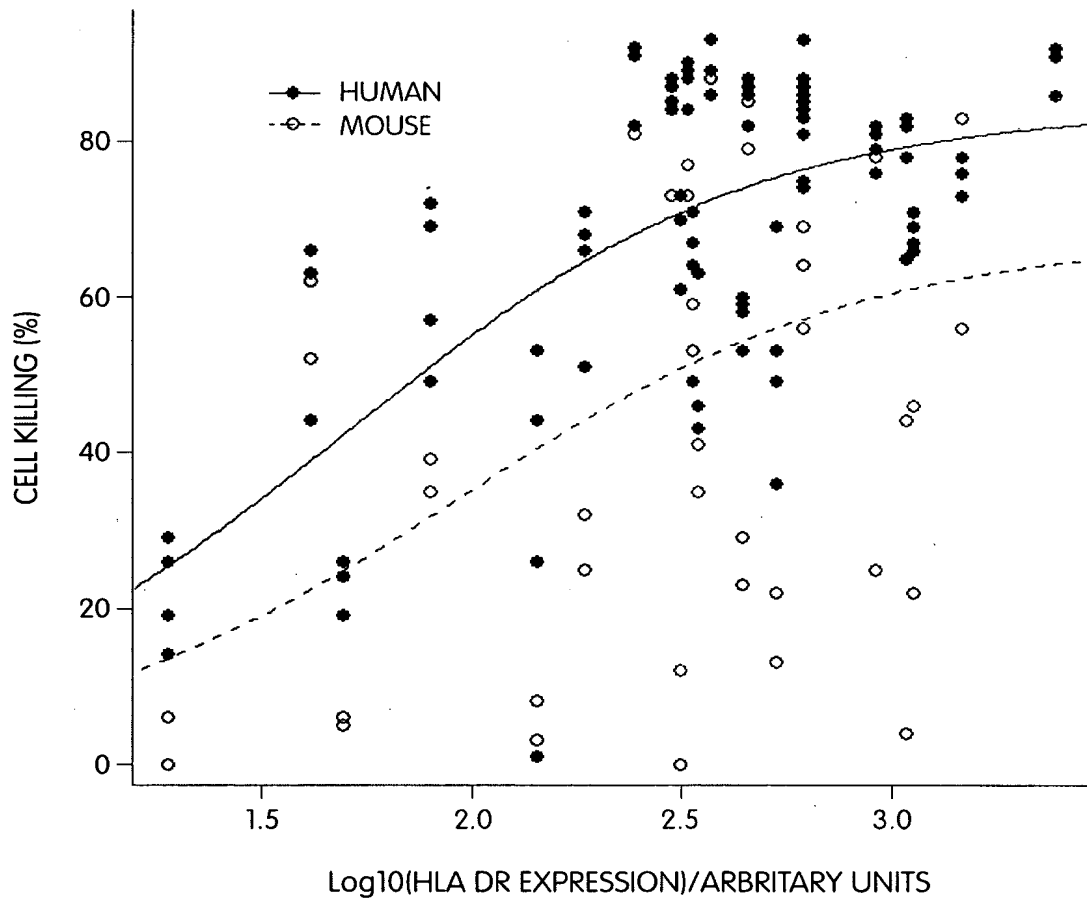


Fig. 4

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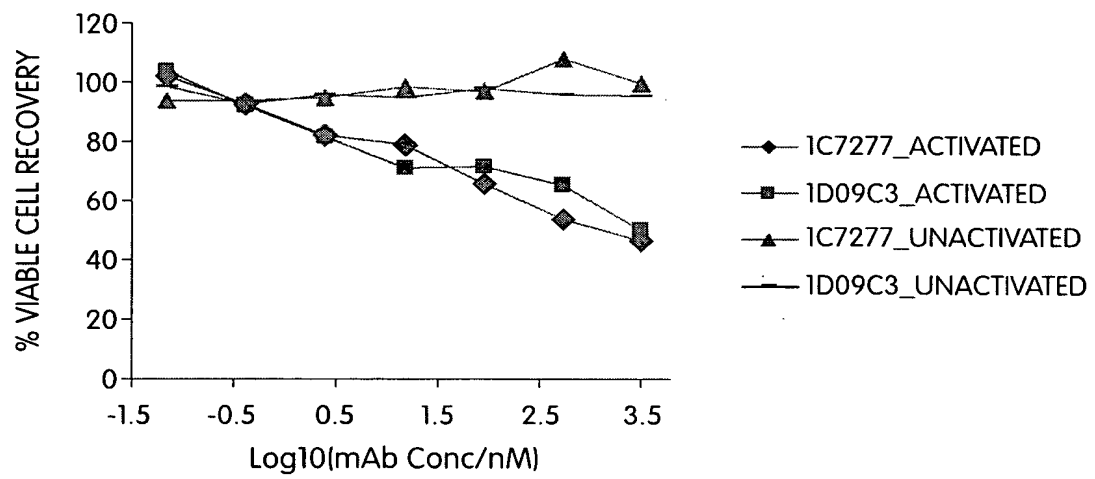


Fig. 5

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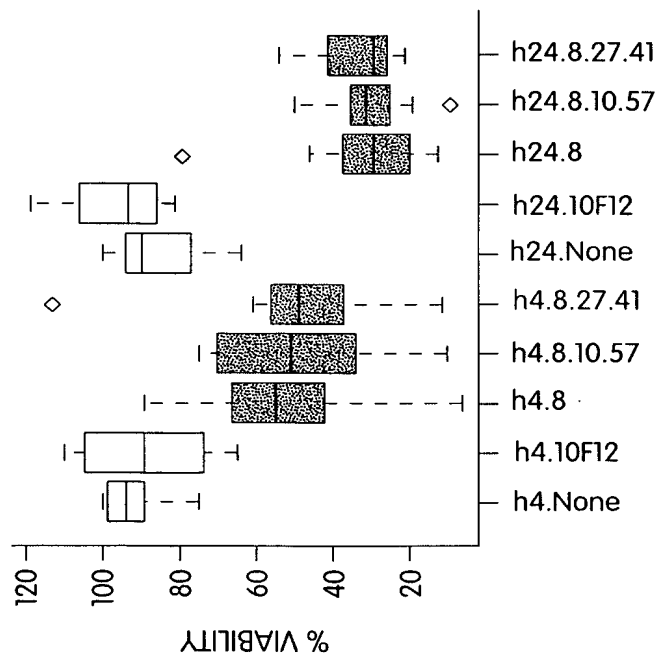
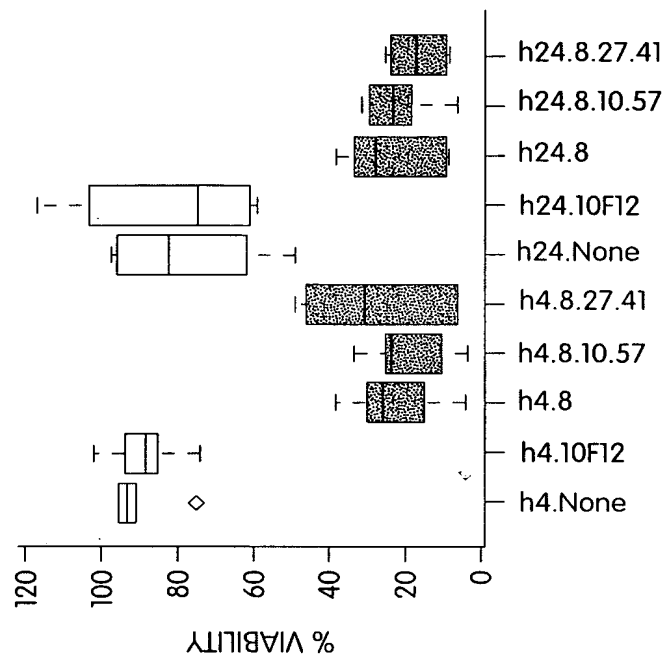


Fig. 6A



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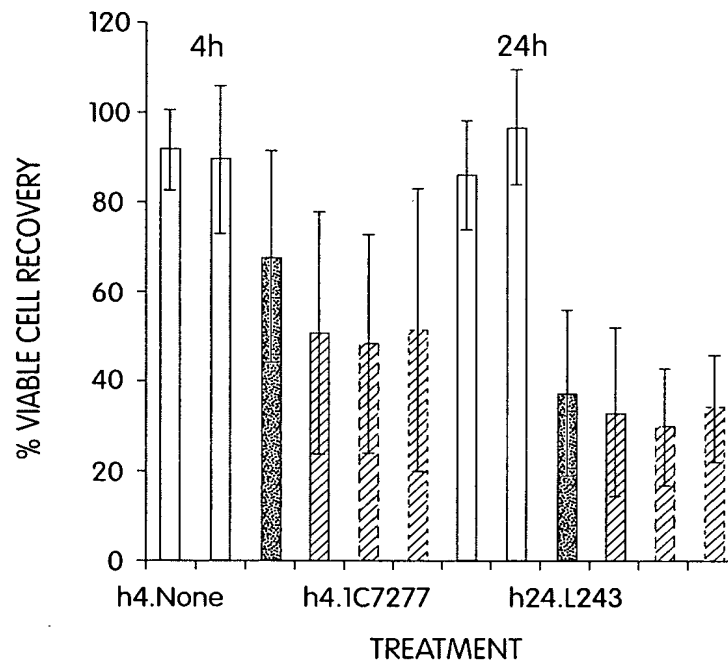


Fig. 6B

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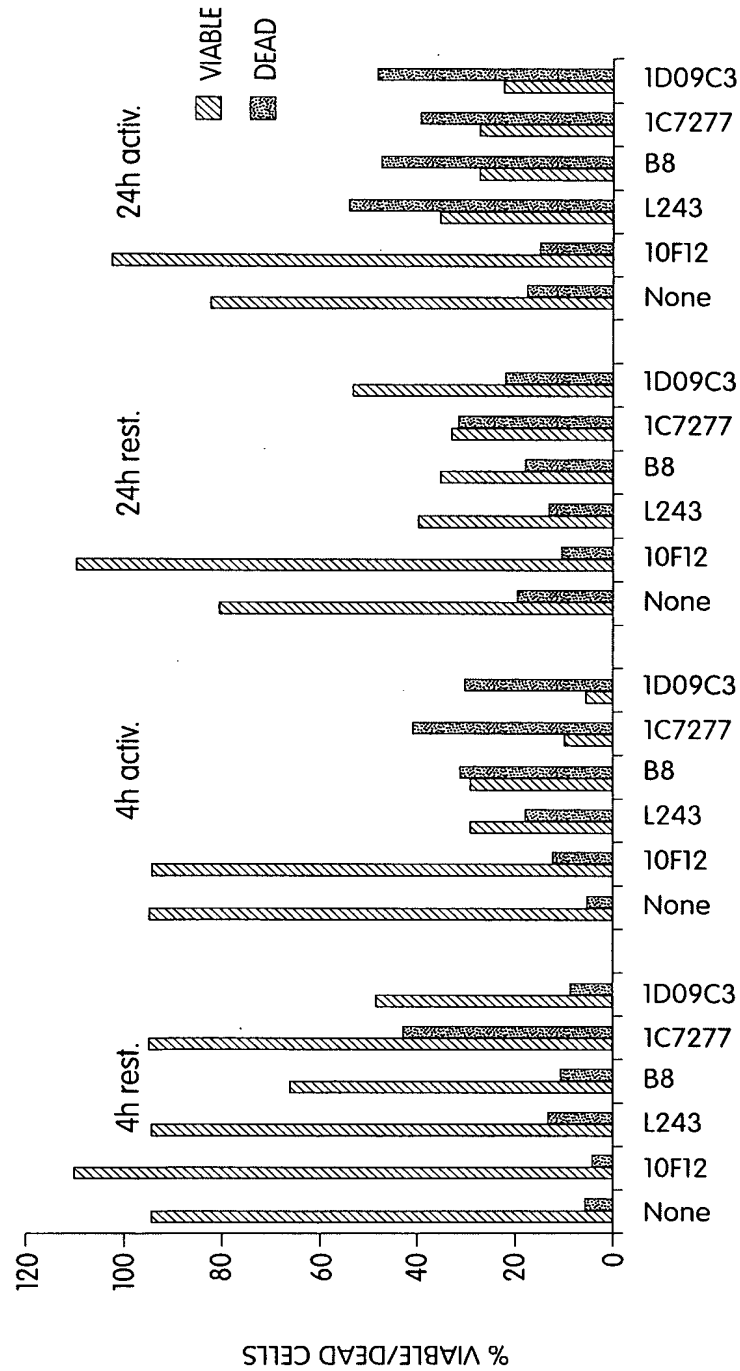


Fig. 6C

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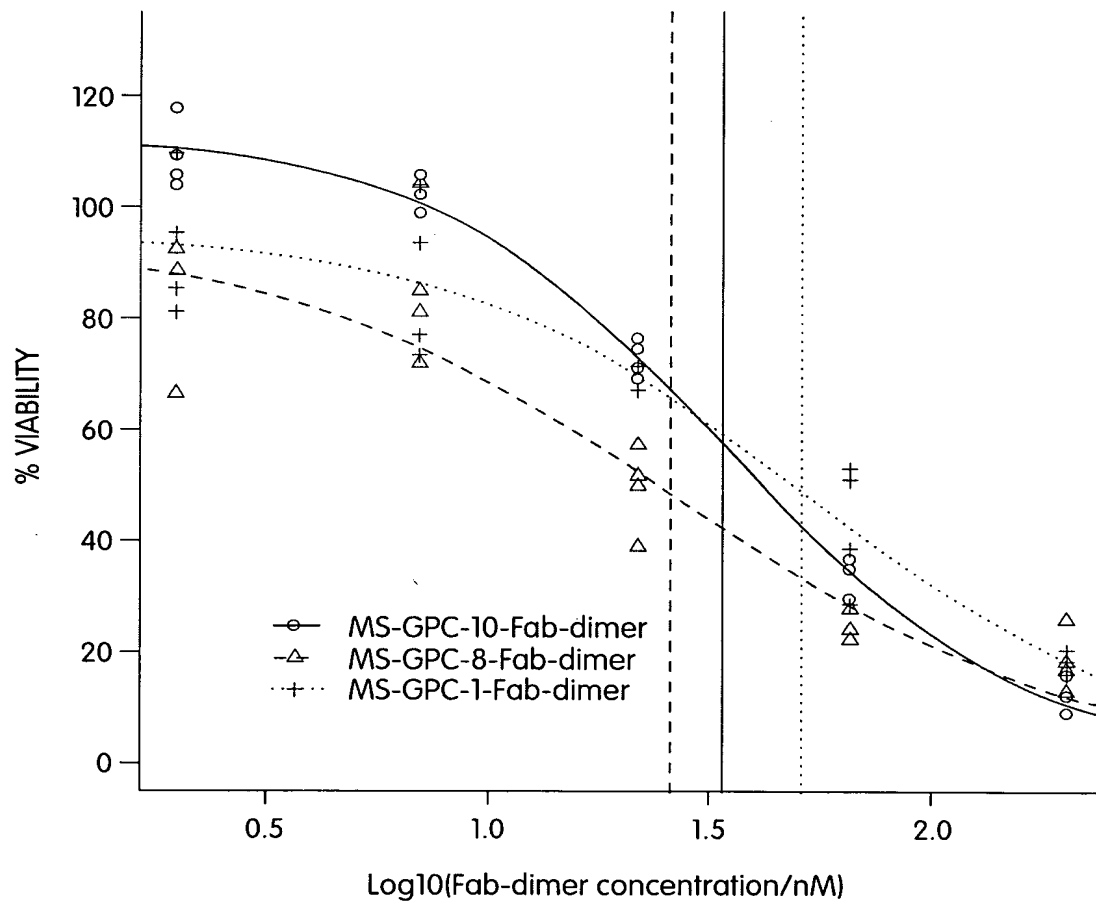


Fig. 7A

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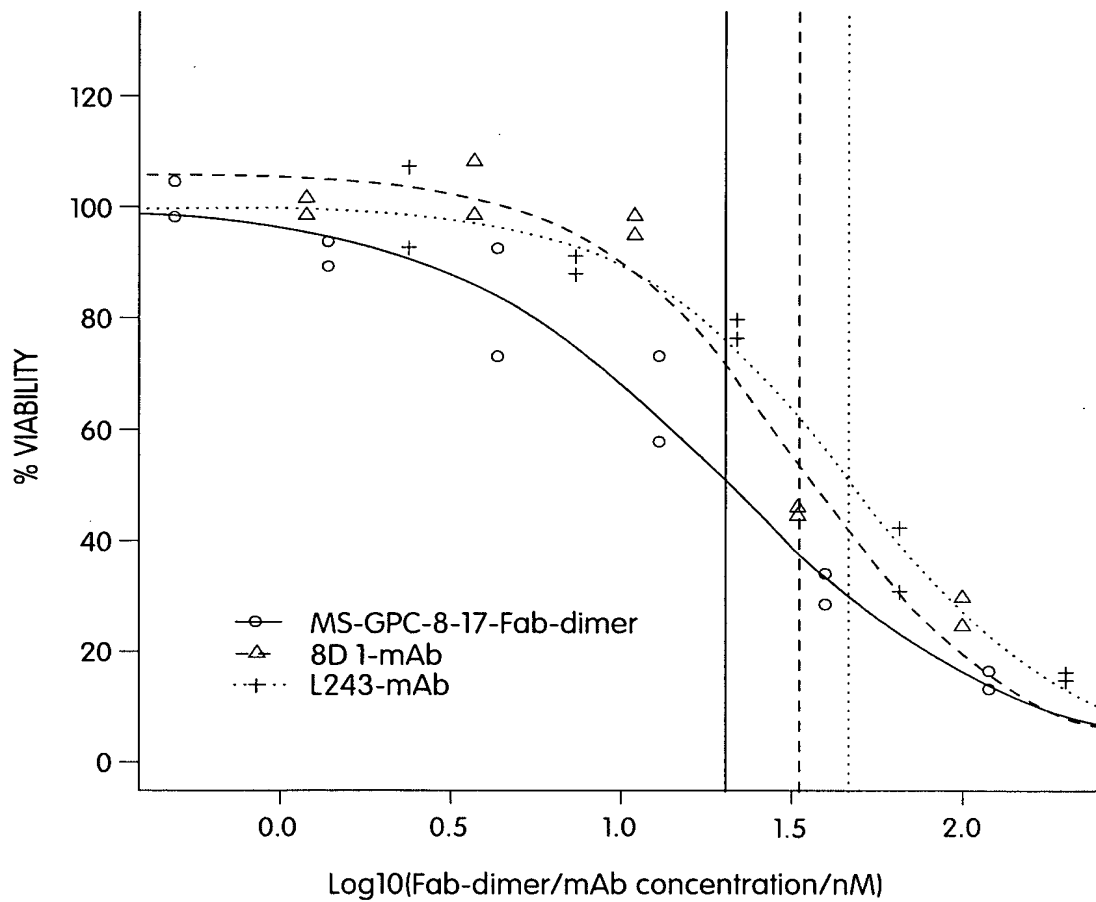


Fig. 7B

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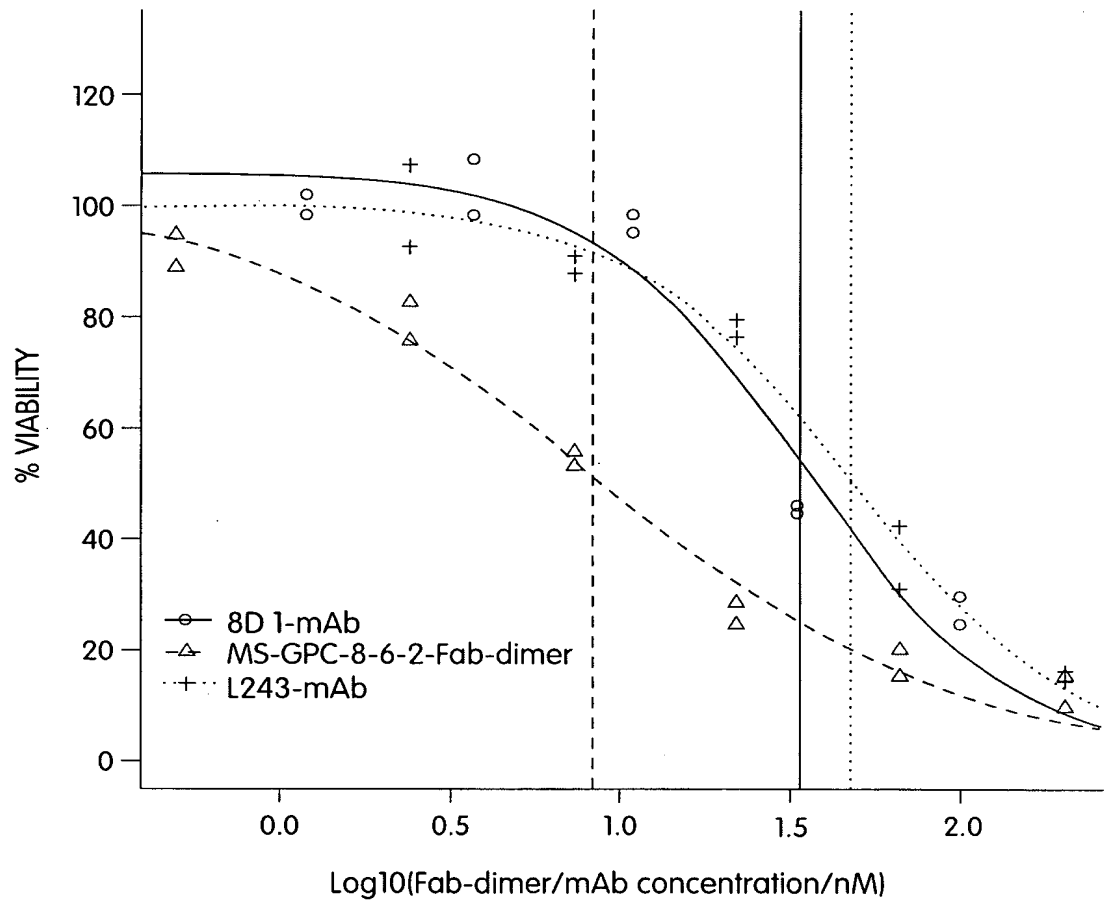


Fig. 7C

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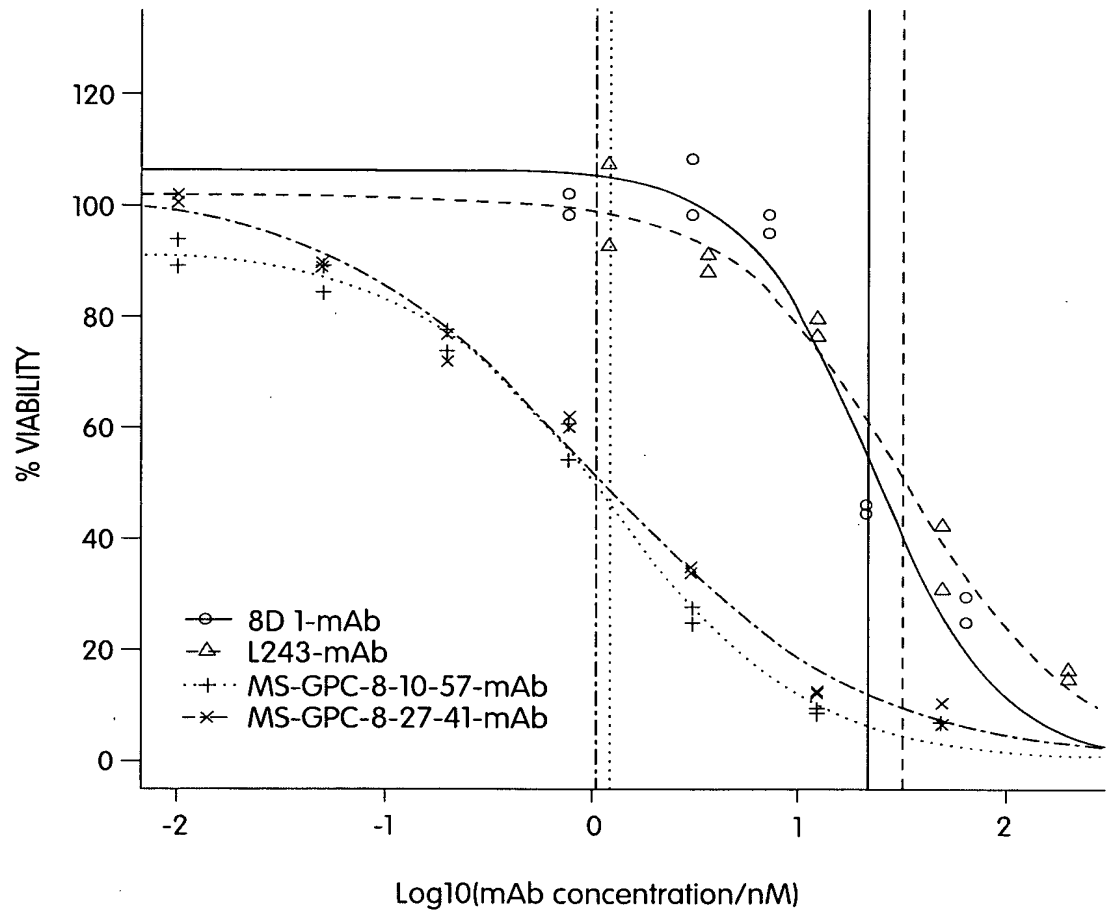


Fig. 7D

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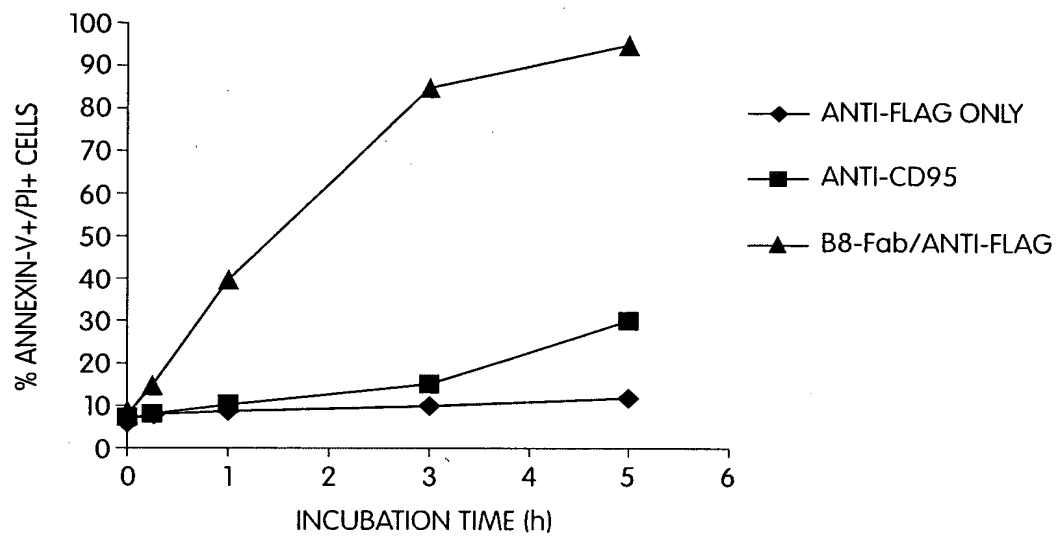


Fig. 8A

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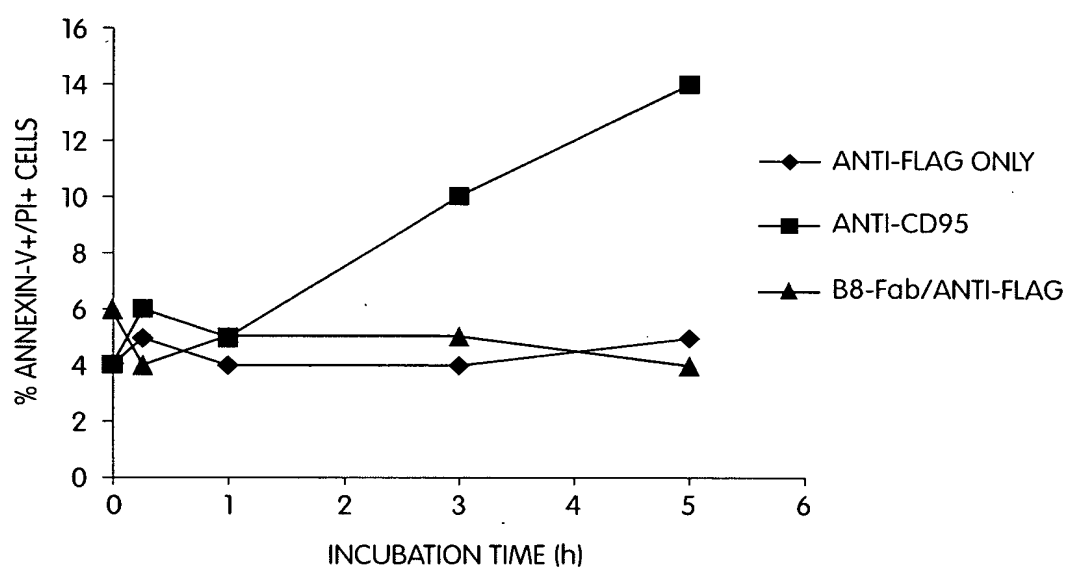


Fig. 8B



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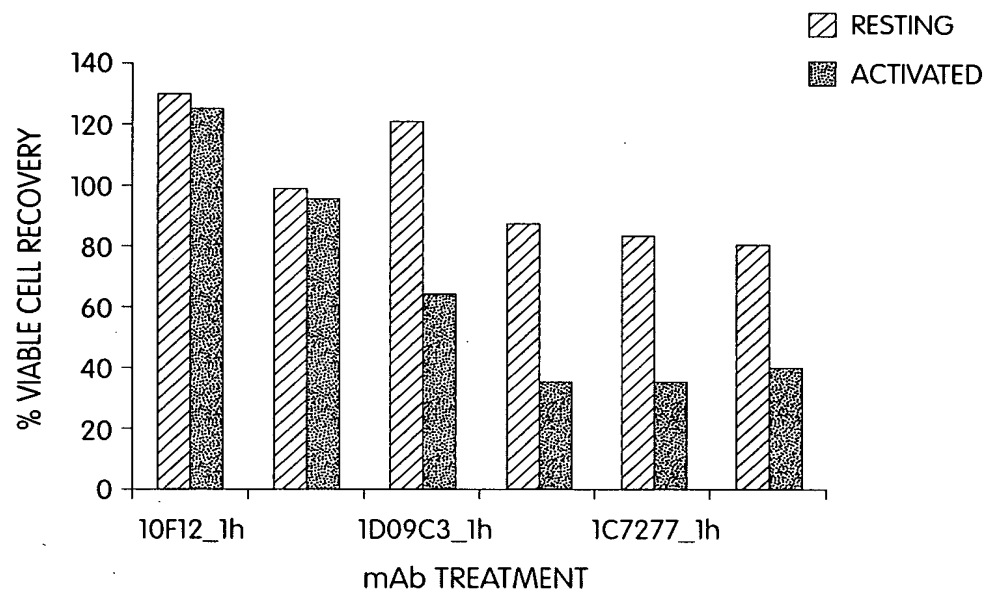


Fig. 8C

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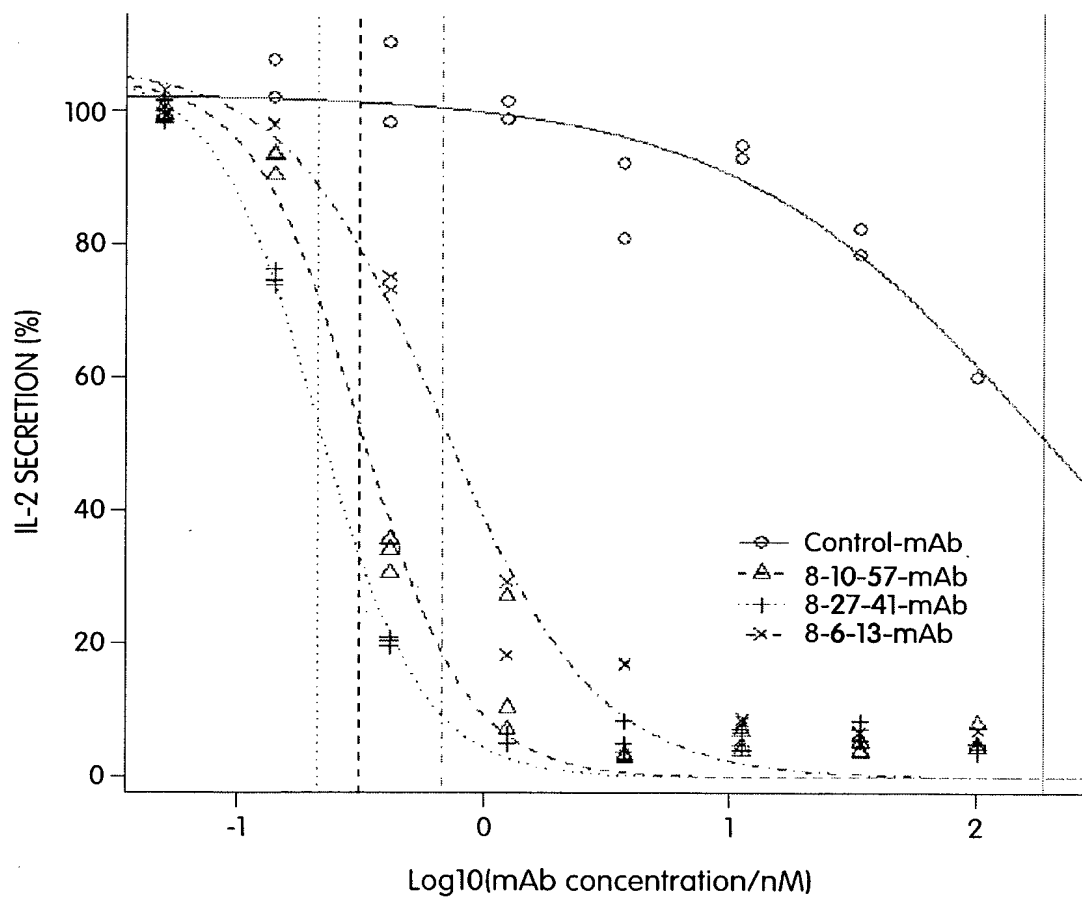


Fig. 9A

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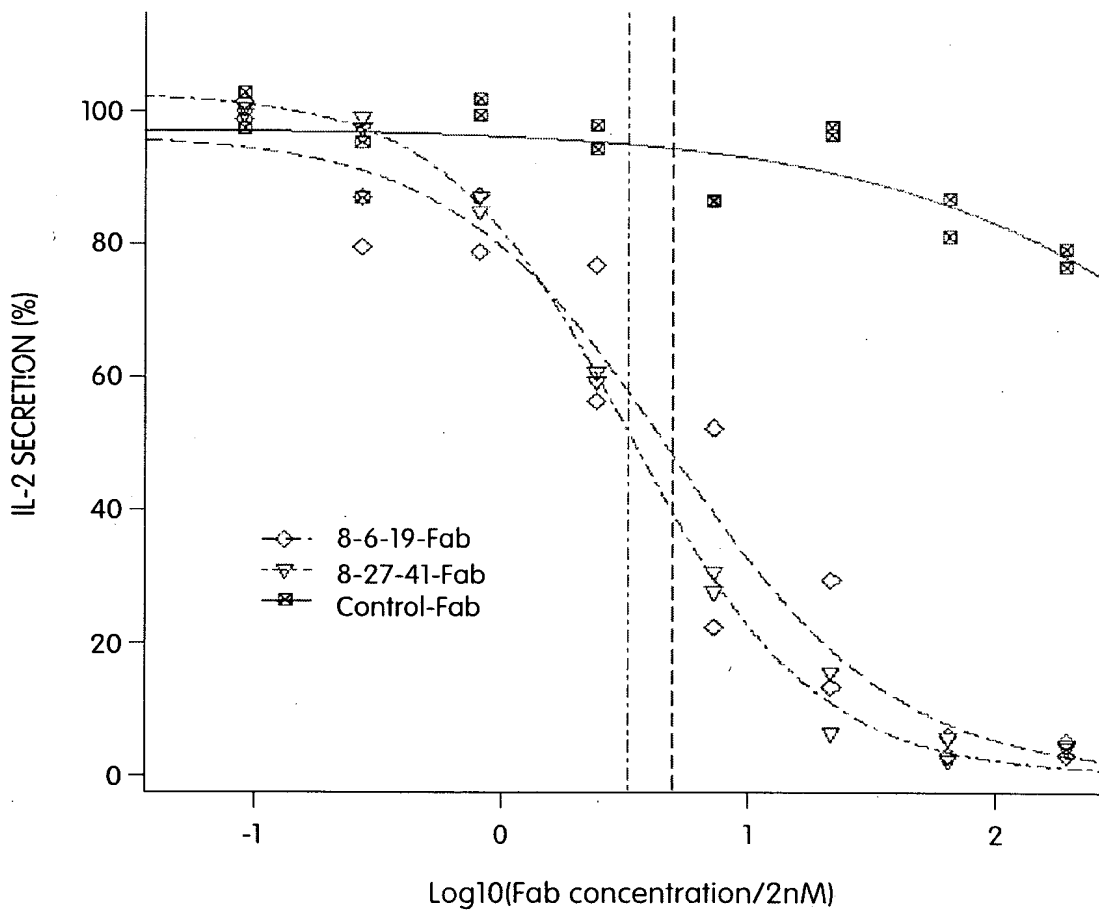


Fig. 9B

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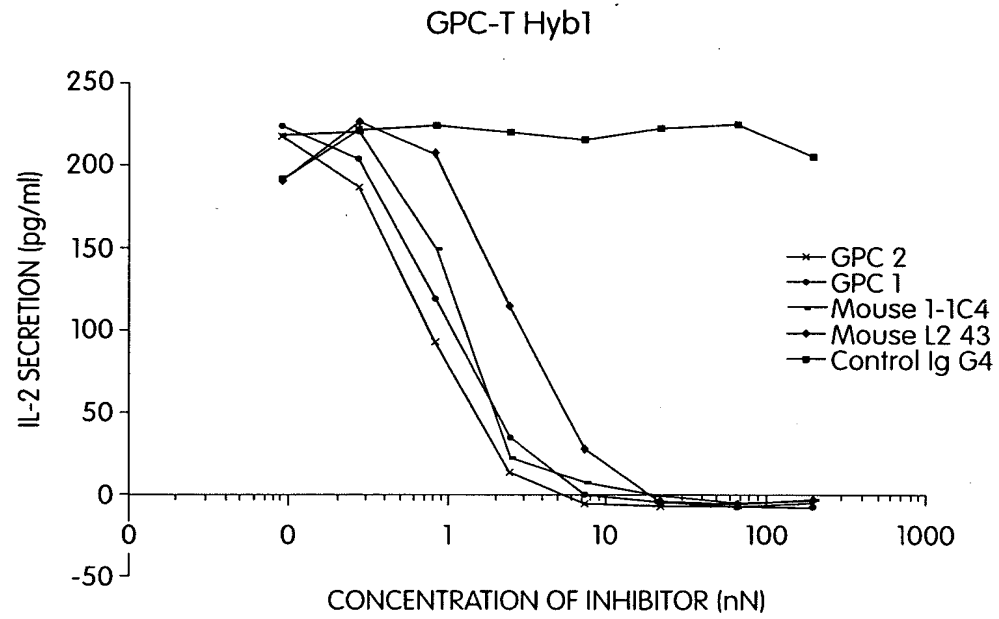
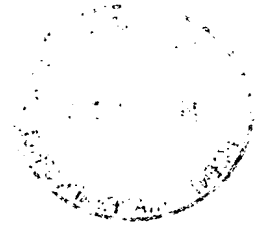


Fig. 9C

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Cell line NG-TcL HA-10

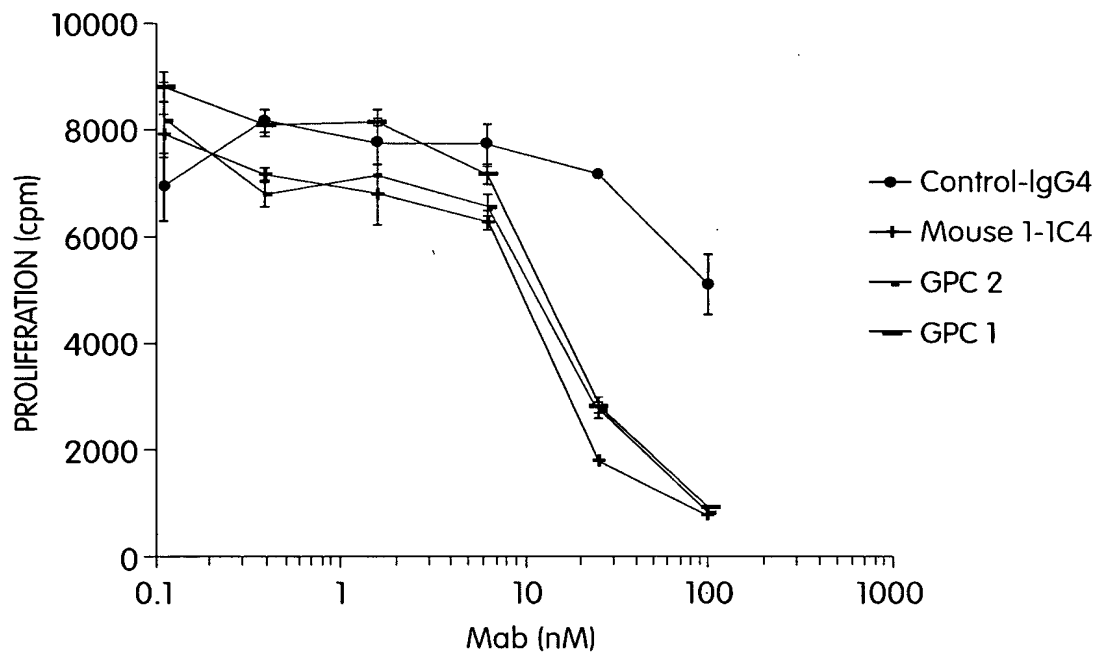


Fig. 9D

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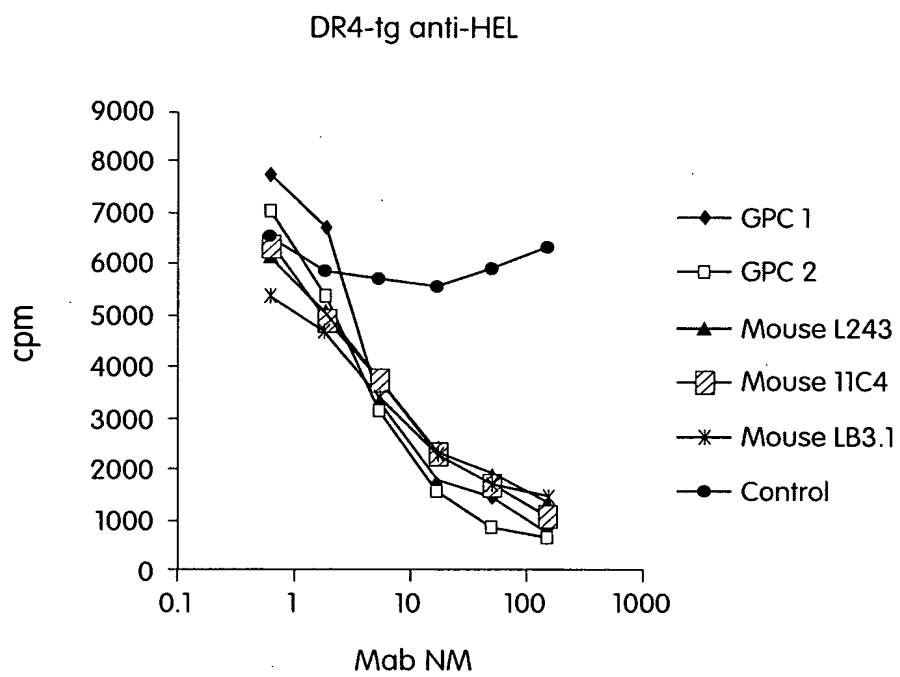


Fig. 9E

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DR14-tg anti-OVA

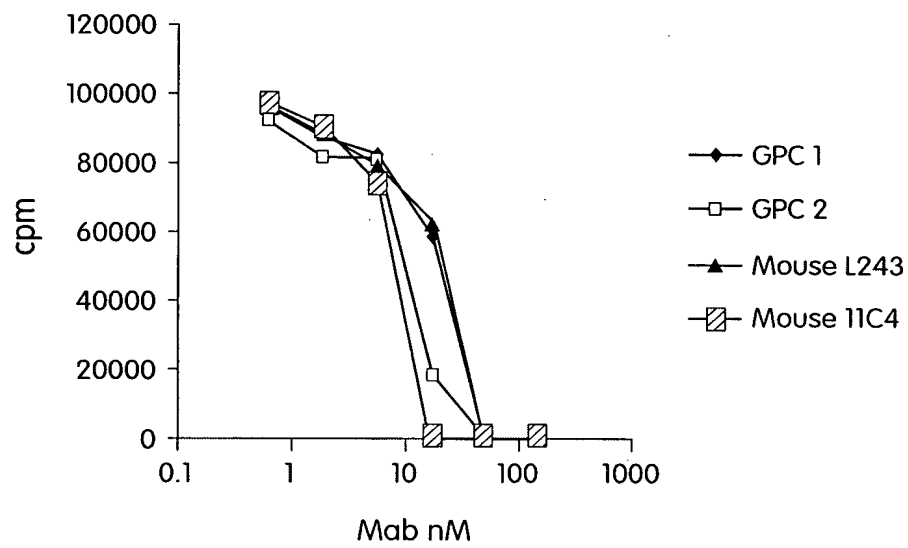
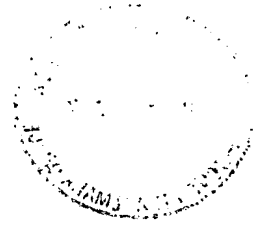
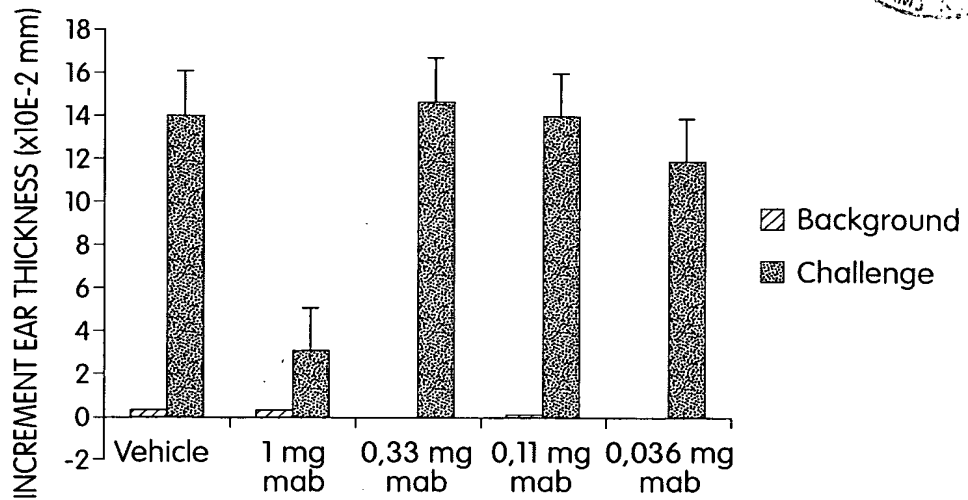


Fig. 9F

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## DTH to OXAZOLONE



## DTH to OXAZOLONE

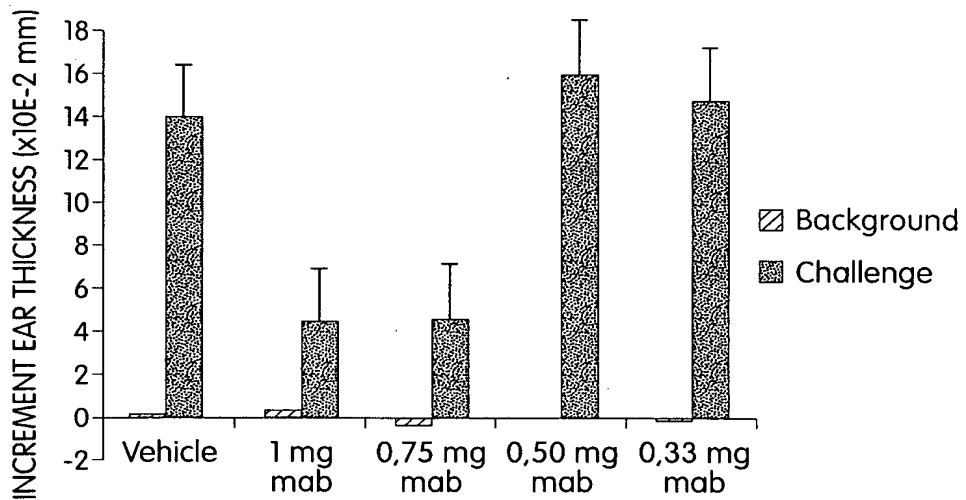


Fig. 9G



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DTH to DNFB

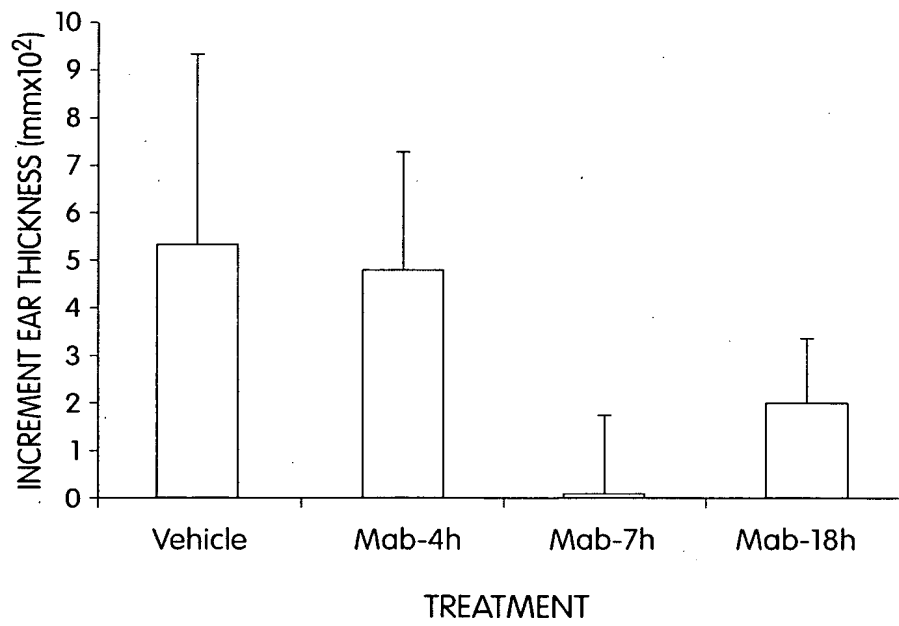
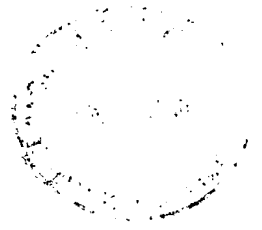


Fig. 9H

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DTH to DNFB

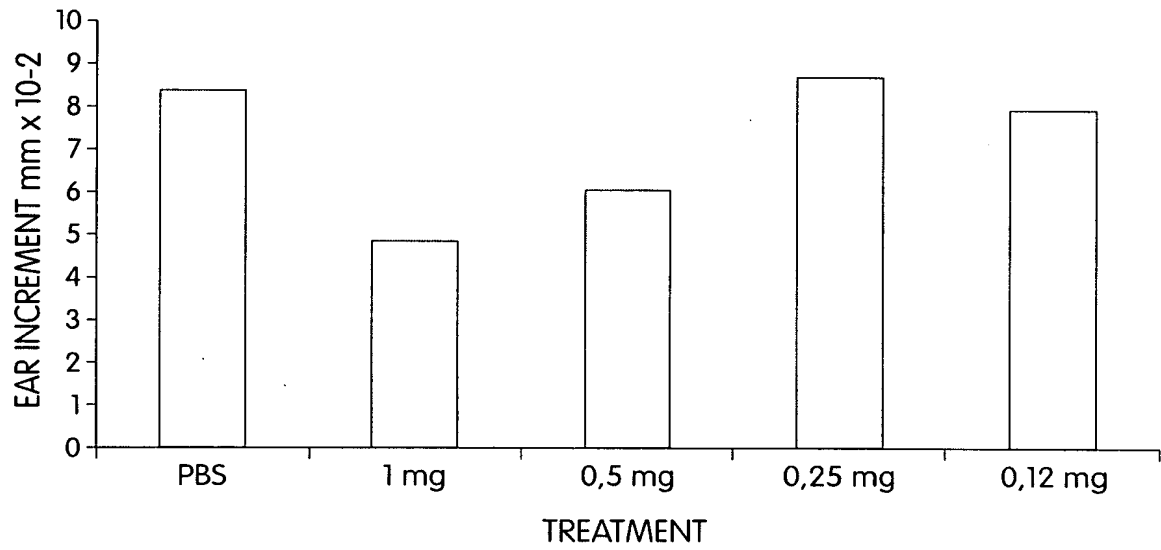


Fig. 9I

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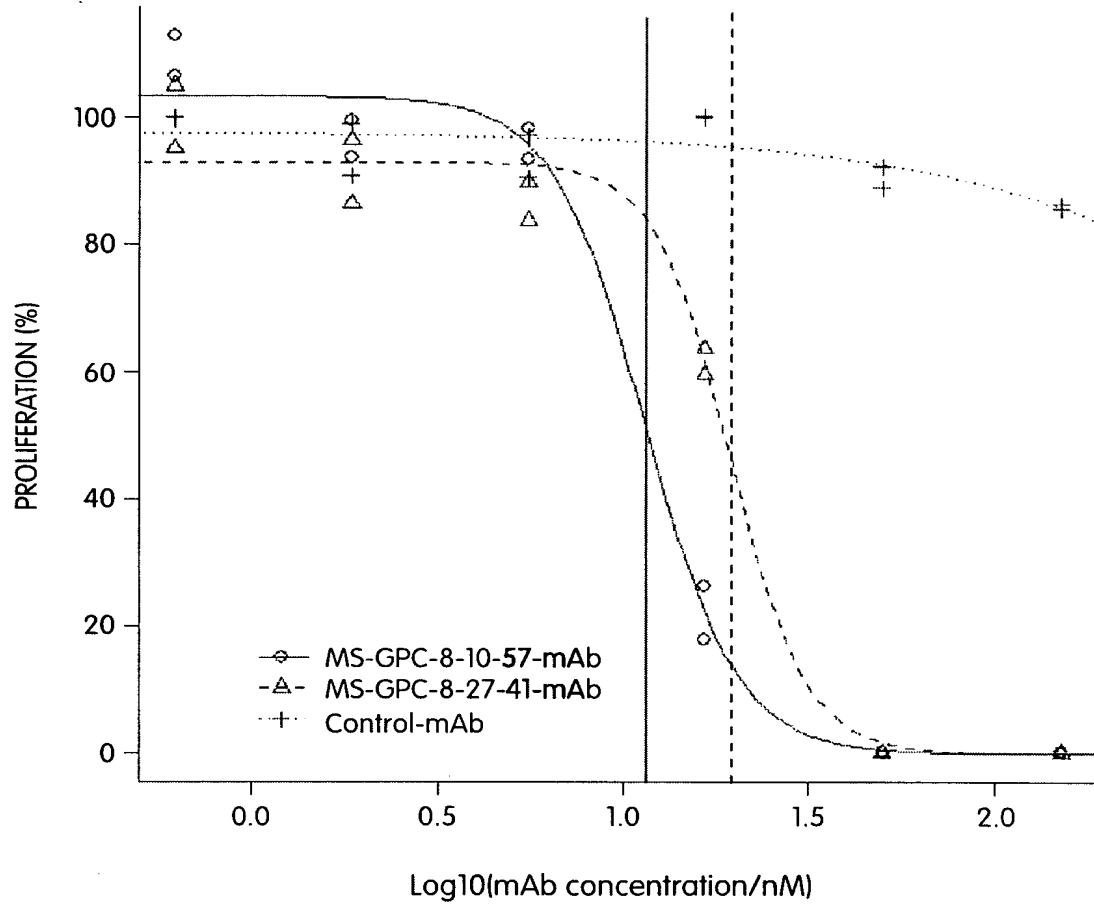
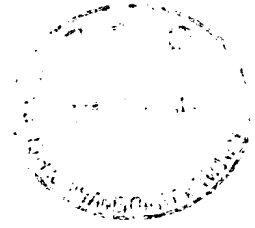


Fig. 10

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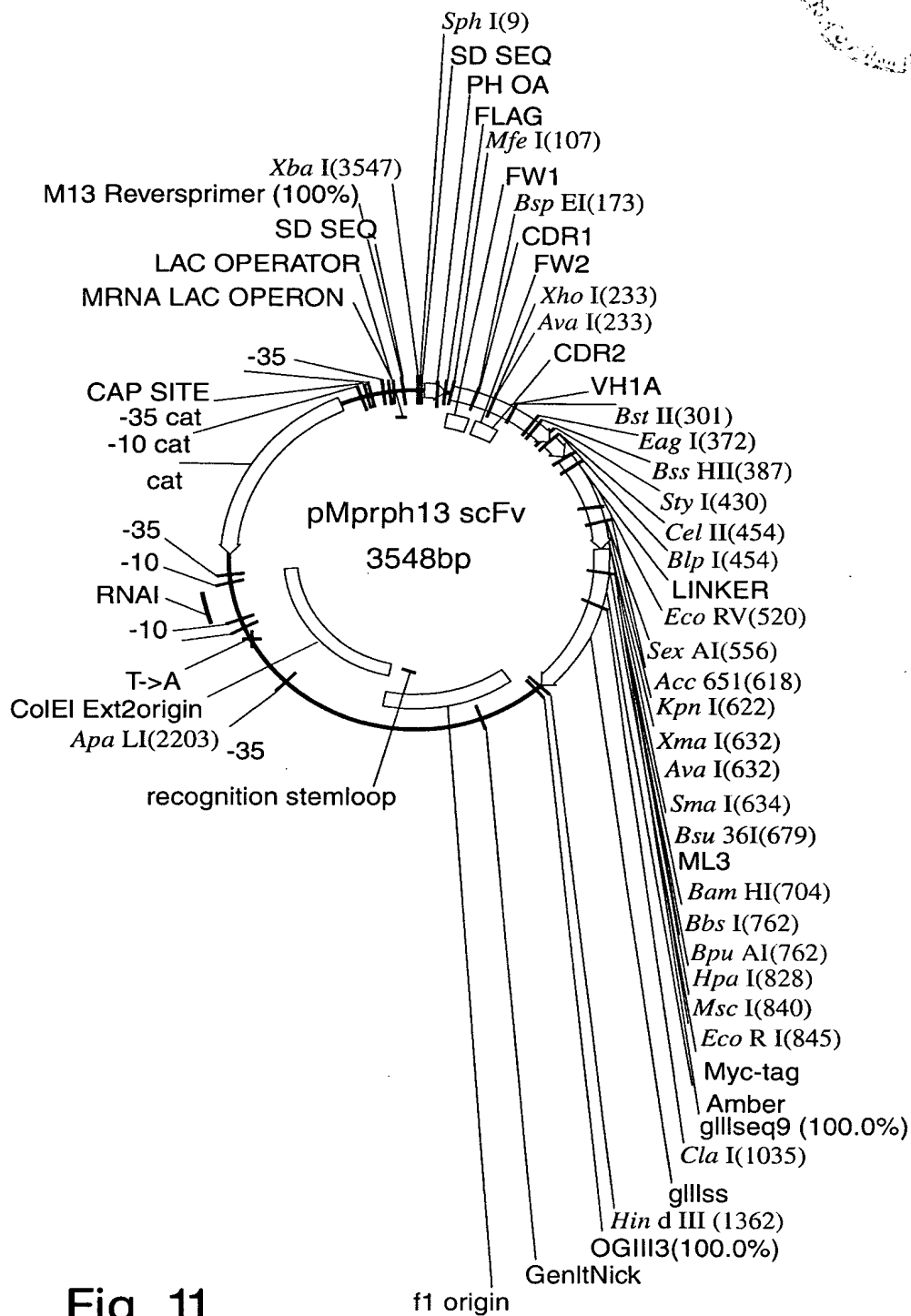



Fig. 11

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**XbaISphI**  
 ~~~~~  
 1 AGAGCATGCG TAGGAGAAAA TAAAATGAAA CAAAGCACTA TTGCACTGGC  
 TCTCGTACGC ATCCTCTTTT ATTTTACTTT GTTTCGTGAT AACGTGACCG  
 51 ACTCTTACCG TTGCTCTTCA CCCCTGTTAC CAAAGCCGAC TACAAAGATG  
 TGAGAATGGC AACGAGAAGT GGGGACAATG GTTTCGGCTG ATGTTTCTAC  
  
**MfeI**  
 ~~~~~  
 101 AAGTGCAATT GGTTCAGTCT GGCGCGGAAG TGAAAAAACC GGGCAGCAGC  
 TTCACGTTAA CCAAGTCAGA CCGCGCCTTC ACTTTTTTGG CCCGTCGTCG  
  
**BspEI**  
 ~~~~~  
 151 GTGAAAGTGA GCTGCAAAGC CTCCGGAGGC ACTTTTAGCA GCTATGCGAT  
 CACTTTTCACT CGACGTTTCG GAGGCCTCCG TGAAAATCGT CGATACGCTA  
  
**XhoI**  
 ~~~~~  
**AvaI**  
 ~~~~~  
 201 TAGCTGGGTG CGCCAAGCCC CTGGGCAGGG TCTCGAGTGG ATGGGCGGCA  
 ATCGACCCAC GCGGTTCGGG GACCCGTCCC AGAGCTCACC TACCCGCCGT  
  
**BstEII**  
 ~~~~~  
 251 TTATTCCGAT TTTTGGCACG GCGAACTACG CGCAGAAGTT TCAGGGCCGG  
 AATAAGGCTA AAAACCGTGC CGCTTGATGC GCGTCTTCAA AGTCCCGGCC  
  
**BstEII**  
 ~~~~~  
 301 GTGACCATTA CCGCGGATGA AAGCACCAGC ACCGCGTATA TGGAAGTGA  
 CACTGGTAAT GCGGCCTACT TTCGTGGTCG TGGCGCATAT ACCTTGACTC  
  
**EagI** **BssHII**  
 ~~~~~ ~~~~~  
 351 CAGCCTGCGT AGCGAAGATA CGGCCGTGTA TTATTGCGCG CGTTATTATG  
 GTCGGACGCA TCGCTTCTAT GCCGGCACAT AATAACGCGC GCAATAATAC  
  
**StyI**  
 ~~~~~  
 401 ATCGTATGTA TAATATGGAT TATTGGGGCC AAGGCACCCT GGTGACGGTT  
 TAGCATACAT ATTATACCTA ATAACCCCGG TTCCGTGGGA CCACTGCCAA  
  
**BlpI**  
 ~~~~~  
**CelII**  
 ~~~~~  
 451 AGCTCAGCGG GTGGCGGTTC TGGCGGCGGT GGGAGCGGTG GCGGTGGTTC

Fig. 11 (cont.)

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TCGAGTCGCC CACCGCCAAG ACCGCCGCCA CCCTCGCCAC CGCCACCAAG

EcoRV

501 TGGCGGTGGT GGTTCGGATA TCGAACTGAC CCAGCCGCCT TCAGTGAGCG  
 ACCGCCACCA CCAAGGCTAT AGCTTGACTG GGTGCGCGGA AGTCACTCGC

SexAI

551 TTGCACCAGG TCAGACCGCG CGTATCTCGT GTAGCGGCGA TGCCTGCGG  
 AACGTGGTCC AGTCTGGCGC GCATAGAGCA CATCGCCGCT ACCTGACCCG

XmaI

~~~~~

KpnI

~~~~~

Acc65I

~~~~~

SmaI

~~~~~

AvaI

~~~~~

601 GATAAATACG CGAGCTGGTA CCAGCAGAAA CCCGGGCAGG CGCCAGTTCT  
 CTATTTATGC GCTCGACCAT GGTGCTCTTT GGGCCCGTCC GCGGTCAAGA

Bsu36I

~~~~~

651 GGTGATTTAT GATGATTCTG ACCGTCCCTC AGGCATCCCG GAACGCTTTA  
 CCACTAAATA CTACTAAGAC TGGCAGGGAG TCCGTAGGGC CTTGCGAAAT

BamHI

~~~~~

701 GCGGATCCAA CAGCGGCAAC ACCGCGACCC TGACCATTAG CGGCACTCAG  
 CGCCTAGGTT GTCGCCGTTG TGGCGCTGGG ACTGGTAATC GCCGTGAGTC

BpuAI

~~~~~

BbsI

~~~~~

751 GCGGAAGACG AAGCGGATTA TTATTGCCAG AGCTATGACG CTCATATGCG  
 CGCCTTCTGC TTCGCCTAAT AATAACGGTC TCGATACTGC GAGTATACGC

HpaI

~~~~~

MscI

~~~~~

EcoRI

~~~~~

801 TCCTGTGTTT GCGGCGGCA CGAAGTTAAC CGTTCTTGGC CAGGAATTCTG  
 AGGACACAAA CCGCCGCCGT GCTTCAATTG GCAAGAACCG GTCCTTAAGC

851 AGCAGAAGCT GATCTCTGAG GAGGATCTGA ACTAGGGTGG TGGCTCTGGT  
 TCGTCTTCGA CTAGAGACTC CTCCTAGACT TGATCCCACC ACCGAGACCA

901 TCCGGTGATT TTGATTATGA AAAGATGGCA AACGCTAATA AGGGGGCTAT  
 AGGCCACTAA AACTAATACT TTTCTACCGT TTGCGATTAT TCCCCGATA

gIIIseq9 100.0%

=====

951 GACCGAAAAT GCCGATGAAA ACGCGCTACA GTCTGACGCT AAAGGCAAAC

Fig. 11 (cont.)

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CTGGCTTTTA CGGCTACTTT TGC GCGATGT CAGACTGCGA TTTCCGTTTG

ClaI

~~~~~

1001 TTGATTCTGT CGCTACTGAT TACGGTGCTG CTATCGATGG TTTTATTGGT  
 AACTAAGACA GCGATGACTA ATGCCACGAC GATAGCTACC AAAGTAACCA

1051 GACGTTTCCG GCCTTGCTAA TGGTAATGGT GCTACTGGTG ATTTTGCTGG  
 CTGCAAAGGC CGGAACGATT ACCATTACCA CGATGACCAC TAAAACGACC

1101 CTCTAATTCC CAAATGGCTC AAGTCGGTGA CGGTGATAAT TCACCTTTAA  
 GAGATTAAGG GTTTACCGAG TTCAGCCACT GCCACTATTA AGTGGAAATT

1151 TGAATAATTT CCGTCAATAT TTACCTTCCC TCCCTCAATC GGTTGAATGT  
 ACTTATTAAA GGCAGTTATA AATGGAAGGG AGGGAGTTAG CCAACTTACA

1201 CGCCCTTTTG TCTTTGGCGC TGGTAAACCA TATGAATTTT CTATTGATTG  
 GCGGGAAAAC AGAAACCGCG ACCATTTGGT ATACTTAAAA GATAACTAAC

1251 TGACAAAATA AACTTATTCC GTGGTGTCTT TCGGTTTCTT TTATATGTTG  
 ACTGTTTAT TTGAATAAGG CACCACAGAA ACGCAAAGAA AATATACAAC

1301 CCACCTTTAT GTATGTATTT TCTACGTTTG CTAACATACT GCGTAATAAG  
 GGTGGAAAATA CATAcataaa AGATGCAAAC GATTGTATGA CGCATTATTC

HindIII

~~~~~

1351 GAGTCTTGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG  
 CTCAGAACTA TTCGAAC TGG ACAC T TCACT TTTTACCGCG TCTAACACGC

OGIII3 100.0%

=====

1401 ACATTTTTTT TGTCTGCCGT TTAATGAAAT TGTAACGTT AATATTTTGT  
 TGTAAAAAAA ACAGACGGCA AATTACTTTA ACATTTGCAA TTATAAAACA

1451 TAAAATTCGC GTTAAATTTT TGTTAAATCA GCTCATTTTT TAACCAATAG  
 ATTTTAAGCG CAATTTAAAA ACAATTTAGT CGAGTAAAAA ATTGGTTATC

1501 GCCGAAATCG GCAAAATCCC TTATAAATCA AAAGAATAGA CCGAGATAGG  
 CGGCTTTAGC CGTTTTAGGG AATATTTAGT TTTCTTATCT GGCTCTATCC

1551 GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG  
 CAACTCACAA CAAGGTCAA CCTTGTTCTC AGGTGATAAT TTCTTGACCC

1601 ACTCCAACGT CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA  
 TGAGGTTGCA GTTTCCCGCT TTTTGGCAGA TAGTCCCGCT ACCGGGTGAT

1651 CGAGAACCAT CACCCTAATC AAGTTTTTTG GGGTCGAGGT GCCGTAAAGC  
 GCTCTTGGTA GTGGGATTAG TTCAAAAAAC CCCAGCTCCA CGGCATTTCG

1701 ACTAAATCGG AACCCCTAAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA  
 TGATTTAGCC TTGGGATTTT CCTCGGGGGC TAAATCTCGA ACTGCCCCCTT

Fig. 11 (cont.)

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1751	AGCCGGCGAA	CGTGGCGAGA	AAGGAAGGGA	AGAAAGCGAA	AGGAGCGGGC
	TCGGCCGCTT	GCACCGCTCT	TTCCTTCCCT	TCTTTCGCTT	TCCTCGCCCC
1801	GCTAGGGCGC	TGGCAAGTGT	AGCGGTCACG	CTGCGCGTAA	CCACCACACC
	CGATCCCGCG	ACCGTTCACA	TCGCCAGTGC	GACGCGCATT	GGTGGTGTGG
1851	CGCCGCGCTT	AATGCGCCGC	TACAGGGCGC	GTGCTAGCCA	TGTGAGCAAA
	GCGGCGCGAA	TTACGCGGCG	ATGTCCCGCG	CACGATCGGT	ACACTCGTTT
1901	AGGCCAGCAA	AAGGCCAGGA	ACCGTAAAAA	GGCCGCGTTG	CTGGCGTTTT
	TCCGGTCGTT	TTCCGGTCCT	TGGCATTTTT	CCGGCGCAAC	GACCGCAAAA
1951	TCCATAGGCT	CCGCCCCCCT	GACGAGCATC	ACAAAAATCG	ACGCTCAAGT
	AGGTATCCGA	GGCGGGGGGA	CTGCTCGTAG	TGTTTTTAGC	TGCGAGTTCA
2001	CAGAGGTGGC	GAAACCCGAC	AGGACTATAA	AGATAACCAGG	CGTTTCCCCC
	GTCTCCACCG	CTTTGGGCTG	TCCTGATATT	TCTATGGTCC	GCAAAGGGGG
2051	TGGAAGCTCC	CTCGTGCGCT	CTCCTGTTCC	GACCCTGCCG	CTTACCGGAT
	ACCTTCGAGG	GAGCACGCGA	GAGGACAAGG	CTGGGACGGC	GAATGGCCTA
2101	ACCTGTCCGC	CTTCTCCCT	TCGGGAAGCG	TGGCGCTTTC	TCATAGCTCA
	TGGACAGGCG	GAAAGAGGGA	AGCCCTTCGC	ACCGCGAAAG	AGTATCGAGT
2151	CGCTGTAGGT	ATCTCAGTTC	GGTGTAGGTC	GTTGCTCCA	AGCTGGGCTG
	GCGACATCCA	TAGAGTCAAG	CCACATCCAG	CAAGCGAGGT	TCGACCCGAC
	ApaLI				
	~~~~~				
2201	TGTGCACGAA	CCCCCGTTC	AGTCCGACCG	CTGCGCCTTA	TCCGGTAACT
	ACACGTGCTT	GGGGGGCAAG	TCAGGCTGGC	GACGCGGAAT	AGGCCATTGA
2251	ATCGTCTTGA	GTCCAACCCG	GTAAGACACG	ACTTATCGCC	ACTGGCAGCA
	TAGCAGAACT	CAGGTTGGGC	CATTCTGTGC	TGAATAGCGG	TGACCGTCGT
2301	GCCACTGGTA	ACAGGATTAG	CAGAGCGAGG	TATGTAGGCG	GTGCTACAGA
	CGGTGACCAT	TGTCCTAATC	GTCTCGCTCC	ATACATCCGC	CACGATGTCT
2351	GTTCTTGAAG	TGGTGGCCTA	ACTACGGCTA	CACTAGAAGA	ACAGTATTTG
	CAAGAACTTC	ACCACCGGAT	TGATGCCGAT	GTGATCTTCT	TGTCATAAAC
2401	GTATCTGCGC	TCTGCTGTAG	CCAGTTACCT	TCGGAAAAAG	AGTTGGTAGC
	CATAGACGCG	AGACGACATC	GGTCAATGGA	AGCCTTTTTT	TCAACCATCG
2451	TCTTGATCCG	GCAAACAAAC	CACCGCTGGT	AGCGGTGGTT	TTTTTGTTTG
	AGAACTAGGC	CGTTTGTTTG	GTGGCGACCA	TCGCCACCAA	AAAAACAAAC
2501	CAAGCAGCAG	ATTACGCGCA	GAAAAAAAGG	ATCTCAAGAA	GATCCTTTGA
	GTTGTCGTC	TAATGCGCGT	CTTTTTTTTCC	TAGAGTTCTT	CTAGGAAACT
2551	TCTTTTCTAC	GGGGTCTGAC	GCTCAGTGGA	ACGAAAACCTC	ACGTTAAGGG

Fig. 11 (cont.)



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	AGAAAAGATG	CCCCAGACTG	CGAGTCACCT	TGCTTTTGAG	TGCAATTCCC
2601	ATTTTGGTCA TAAAACCAGT	GATCTAGCAC CTAGATCGTG	CAGGCGTTTA GTCCGCAAAT	AGGGCACCAA TCCCGTGGTT	TAAGTGCCTT ATTGACGGAA
2651	AAAAAAATTA TTTTTTTAAAT	CGCCCCGCCC GCGGGGCGGG	TGCCACTCAT ACGGTGAGTA	CGCAGTACTG GCGTCATGAC	TTGTAATTCA AACATTAAAGT
2701	TTAAGCATTG AATTCGTAAG	TGCCGACATG ACGGCTGTAC	GAAGCCATCA CTTCGGTAGT	CAAACGGCAT GTTTGCCGTA	GATGAACCTG CTACTTGAC
2751	AATCGCCAGC TTAGCGGTCG	GGCATCAGCA CCGTAGTCGT	CCTTGTCGCC GGAACAGCGG	TTGCGTATAA AACGCATATT	TATTTGCCCA ATAAACGGGT
2801	TAGTGAAAAC ATCACTTTTG	GGGGGCGAAG CCCCCGCTTC	AAGTTGTCCA TTCAACAGGT	TATTGGCTAC ATAACCGATG	GTTTAAATCA CAAATTTAGT
2851	AAACTGGTGA TTTGACCACT	AACTCACCCA TTGAGTGGGT	GGGATTGGCT CCCTAACCGA	GAGACGAAAA CTCTGCTTTT	ACATATTCTC TGTATAAGAG
2901	AATAAACCTT TTATTTGGGA	TTAGGGAAAT AATCCCTTTA	AGGCCAGGTT TCCGGTCCAA	TTCACCGTAA AAGTGGCATT	CACGCCACAT GTGCGGTGTA
2951	CTTGCGAATA GAACGCTTAT	TATGTGTAGA ATACACATCT	AACTGCCGGA TTGACGGCCT	AATCGTCGTG TTAGCAGCAC	GTATTCACCTC CATAAGTGAG
3001	CAGAGCGATG GTCTCGCTAC	AAAACGTTTC TTTTGCAAAG	AGTTTGCTCA TCAAACGAGT	TGGAAAACGG ACCTTTTGCC	TGTAACAAGG ACATTGTTCC
3051	GTGAACACTA CACTTGTGAT	TCCCATATCA AGGGTATAGT	CCAGCTCACC GGTCGAGTGG	GTCTTTCATT CAGAAAGTAA	GCCATACGGA CGGTATGCCT
3101	ACTCCGGGTG TGAGGCCAC	AGCATTATC TCGTAAGTAG	AGGCGGGCAA TCCGCCCGTT	GAATGTGAAT CTTACACTTA	AAAGGCCGGA TTTCCGGCCT
3151	TAAAACTTGT ATTTTGAACA	GCTTATTTTT CGAATAAAAA	CTTTACGGTC GAAATGCCAG	TTTAAAAAGG AAATTTTTC	CCGTAATATC GGCATTATAG
3201	CAGCTGAACG GTCGACTTGC	GTCTGGTTAT CAGACCAATA	AGGTACATTG TCCATGTAAC	AGCAACTGAC TCGTTGACTG	TGAAATGCCT ACTTTACGGA
3251	CAAAATGTTC GTTTTACAAG	TTTACGATGC AAATGCTACG	CATTGGGATA GTAACCTTAT	TATCAACGGT ATAGTTGCCA	GGTATATCCA CCATATAGGT
3301	GTGATTTTTT CACTAAAAAA	TCTCCATTTT AGAGGTAAAA	AGCTTCCTTA TCGAAGGAAT	GCTCCTGAAA CGAGGACTTT	ATCTCGATAA TAGAGCTATT
3351	CTCAAAAAAT GAGTTTTTTA	ACGCCCGGTA TGCGGGCCAT	GTGATCTTAT CACTAGAATA	TTCATTATGG AAGTAATACC	TGAAAGTTGG ACTTTCAACC
3401	AACCTCACCC TTGGAGTGCG	GACGTCTAAT CTGCAGATTA	GTGAGTTAGC CACTCAATCG	TCACTCATTA AGTGAGTAAT	GGCACCCAG CCGTGGGGTC

Fig. 11 (cont.)

34/57



3451 GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG  
CGAAATGTGA AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC

M13 Reverse primer 100.0%

XbaI

=====

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3501 ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATTTCT  
TATTGTTAAA GTGTGTCCTT TGTCGATACT GGTACTAATG CTTAAAGA

Fig. 11 (cont.)

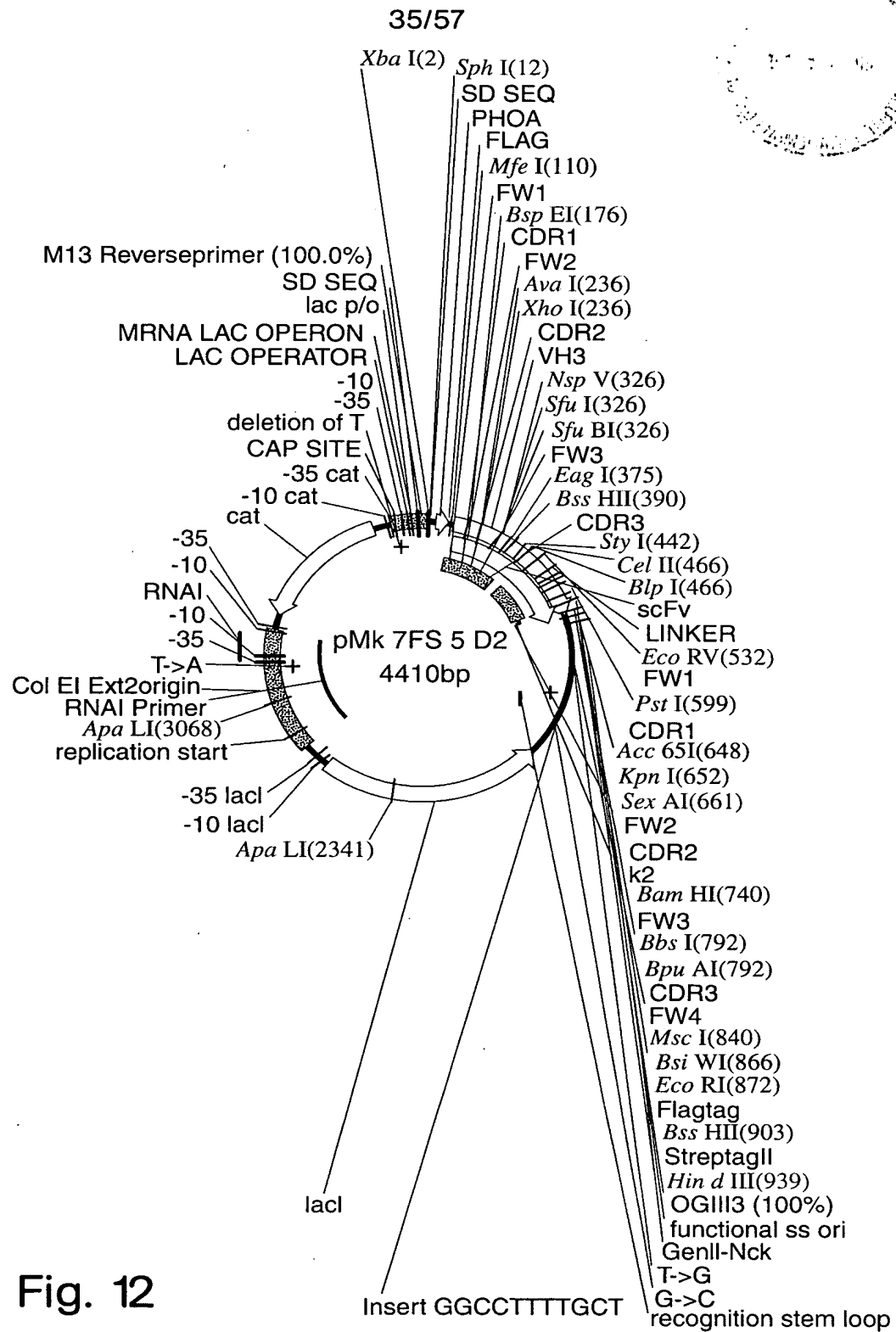


Fig. 12

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XbaI SphI  
~~~~~

1 TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT  
AGATCTCGTA CGCATCCTCT TTTATTTTAC TTTGTTTCGT GATAACGTGA

51 GGCACCTCTTA CCGTTGCTCT TCACCCCTGT TACCAAAGCC GACTACAAAG  
CCGTGAGAAT GGCAACGAGA AGTGGGGACA ATGGTTTCGG CTGATGTTTC

MfeI  
~~~~~

101 ATGAAGTGCA ATTGGTGGAA AGCGGCGGCG GCCTGGTGCA ACCGGGCGGC  
TACTTCACGT TAACCACCTT TCGCCGCCGC CGGACCACGT TGGCCCGCCG

BspEI  
~~~~~

151 AGCCTGCGTC TGAGCTGCGC GGCCTCCGGA TTTACCTTTA GCAGCTATGC  
TCGGACGCAG ACTCGACGCG CCGGAGGCCT AAATGGAAAT CGTCGATACG

XhoI  
~~~~~  
AvaI  
~~~~~

201 GATGAGCTGG GTGCGCCAAG CCCCTGGGAA GGGTCTCGAG TGGGTGAGCG  
CTACTCGACC CACGCGGTTC GGGGACCCTT CCCAGAGCTC ACCCACTCGC

251 CGATTAGCGG TAGCGGCGGC AGCACCTATT ATGCGGATAG CGTGAAAGGC  
GCTAATCGCC ATCGCCGCCG TCGTGGATAA TACGCCTATC GCACCTTCCG

BstBI  
~~~~~  
SfuI  
~~~~~  
NspV  
~~~~~

301 CGTTTTACCA TTTCACGTGA TAATTCGAAA AACACCCTGT ATCTGCAAAT  
GCAAAATGGT AAAGTGCACT ATTAAGCTTT TTGTGGGACA TAGACGTTTA

EagI BssHII  
~~~~~


351 GAACAGCCTG CGTGCGGAAG ATACGGCCGT GTATTATTGC GCGCGTGTTA  
CTTGTCGGAC GCACGCCTTC TATGCCGGCA CATAATAACG CGCGCACAAT

StyI  
~~~~~

401 AGAAGCATTT TTCTCGTAAG AATTGGTTTG ATTATTGGGG CCAAGGCACC  
TCTTCGTAAA AAGAGCATTC TTAACCAAAC TAATAACCCC GGTTCGTTGG

Fig. 12 (cont.)

37/57



B1pI  
 ~~~~~  
 CelIII  
 ~~~~~

451 CTGGTGACGG TTAGCTCAGC GGGTGGCGGT TCTGGCGGCG GTGGGAGCGG  
 GACCACTGCC AATCGAGTCG CCCACCGCCA AGACCGCCGC CACCCCTCGCC

EcoRV  
 ~~~~~

501 TGGCGGTGGT TCTGGCGGTG GTGGTTCCGA TATCGTGATG ACCCAGAGCC  
 ACCGCCACCA AGACCGCCAC CACCAAGGCT ATAGCACTAC TGGGTCTCGG

PstI  
 ~~~~~

551 CACTGAGCCT GCCAGTGACT CCGGGCGAGC CTGCGAGCAT TAGCTGCAGA  
 GTGACTCGGA CGGTCCTGA GGCCCGCTCG GACGCTCGTA ATCGACGTCT

KpnI  
 ~~~~~  
 Acc65I  
 ~~~~~

601 AGCAGCCAAA GCCTGCTGCA TAGCAACGGC TATAACTATC TGGATTGGTA  
 TCGTCGGTTT CGGACGACGT ATCGTTGCCG ATATTGATAG ACCTAACCAT

KpnI  
 ~~~  
 Acc65I      SexAI  
 ~~~~~

651 CCTTCAAAAA CCAGGTCAAA GCGGCGCAGCT ATTAATTTAT CTGGGCAGCA  
 GGAAGTTTTT GGTCCAGTTT CGGGCGTCGA TAATTAAATA GACCCGTCGT

BamHI  
 ~~~~~

701 ACCGTGCCAG TGGGGTCCCG GATCGTTTTA GCGGCTCTGG ATCCGGCACC  
 TGGCACGGTC ACCCCAGGGC CTAGCAAAAT CGCCGAGACC TAGGCCGTGG

BpuAI  
 ~~~~~  
 BbsI  
 ~~~~~

751 GATTTTACCC TGAAAATTAG CCGTGTGGAA GCTGAAGACG TGGGCGTGTA  
 CTAAAATGGG ACTTTTAATC GGCACACCTT CGACTTCTGC ACCCGCACAT

MscI  
 ~~~~~

801 TTATTGCCAG CAGCATTATA CCACCCCGCC GACCTTTGGC CAGGGTACGA  
 AATAACGGTC GTCGTAATAT GGTGGGGCGG CTGGAAACCG GTCCCATGCT

Fig. 12 (cont.)

**BsiWI      EcoRI**

**BssHII**

HindIII

OGIII3 100.0%

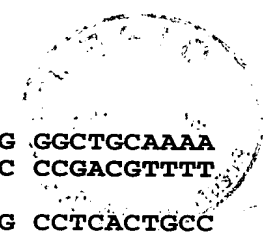
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OGIII3 100.0

**Abstract**

1451 GCGTAACCAC CACACCCGCC GCGCTTAATG CGCCGCTACA GGGCGCGTGC  
CGCATTGGTG GTGTGGGCGG CGCGAATTAC GCGGCGATGT CCCGCGCACG

39/57



1501	TAGACTAGTG ATCTGATCAC	TTTAAACCGG AAATTTGGCC	ACCGGGGGGG TGGCCCCCCC	GGCTTAAGTG CCGAATTCAC	GGCTGCAAAA CCGACGTTT
1551	CAAAACGGCC GTTTTGCCGG	TCCTGTCAGG AGGACAGTCC	AAGCCGCTTT TTCGGCGAAA	TATCGGGTAG ATAGCCCATC	CCTCACTGCC GGAGTGACGG
1601	CGCTTTCCAG GCGAAAGGTC	TCGGGAAACC AGCCCTTTGG	TGTCGTGCCA ACAGCACGGT	GCTGCATCAG CGACGTAGTC	TGAATCGGCC ACTTAGCCGG
1651	AACGCGCGGG TTGCGCGCCC	GAGAGGCGGT CTCTCCGCCA	TTGCGTATTG AACGCATAAC	GGAGCCAGGG CCTCGGTCCC	TGGTTTTTCT ACCAAAAAGA
1701	TTTCACCAGT AAAGTGGTCA	GAGACGGGCA CTCTGCCCCG	ACAGCTGATT TGTCGACTAA	GCCCTTCACC CGGGAAGTGG	GCCTGGCCCT CGGACCGGGA
1751	GAGAGAGTTG CTCTCTCAAC	CAGCAAGCGG GTCGTTCGCC	TCCACGCTGG AGGTGCGACC	TTTGCCCCAG AAACGGGGTC	CAGGCGAAAA GTCCGCTTTT
1801	TCCTGTTTGA AGGACAAACT	TGGTGGTCAG ACCACCAGTC	CGGCGGGATA GCCGCCCTAT	TAACATGAGC ATTGTACTCG	TGTCCTCGGT ACAGGAGCCA
1851	ATCGTCGTAT TAGCAGCATA	CCCACTACCG GGGTGATGGC	AGATGTCCGC TCTACAGGCG	ACCAACGCGC TGGTTGCGCG	AGCCCGGACT TCGGGCCTGA
1901	CGGTAATGGC GCCATTACCG	ACGCATTGCG TGCCTAACGC	CCCAGCGCCA GGGTGCGGGT	TCTGATCGTT AGACTAGCAA	GGCAACCAGC CCGTTGGTCG
1951	ATCGCAGTGG TAGCGTCACC	GAACGATGCC CTTGCTACGG	CTCATTCAGC GAGTAAGTCG	ATTTGCATGG TAAACGTACC	TTTGTGAAA AAACAACTTT
2001	ACCGGACATG TGGCCTGTAC	GCACTCCAGT CGTGAGGTCA	CGCCTTCCCG GCGGAAGGGC	TTCCGCTATC AAGGCGATAG	GGCTGAATTT CCGACTTAAA
2051	GATTGCGAGT CTAACGCTCA	GAGATATTTA CTCTATAAAT	TGCCAGCCAG ACGGTCGGTC	CCAGACGCAG GGTCTGCGTC	ACGCGCCGAG TGCGCGGCTC
2101	ACAGAACTTA TGTCCTGAAT	ATGGGCCAGC TACCCGGTCC	TAACAGCGCG ATTGTCGCGC	ATTTGCTGGT TAAACGACCA	GGCCCAATGC CCGGGTACG
2151	GACCAGATGC CTGGTCTACG	TCCACGCCCCA AGGTGCGGGT	GTCGCGTACC CAGCGCATGG	GTCCTCATGG CAGGAGTACC	GAGAAAATAA CTCTTTTATT
2201	TACTGTTGAT ATGACAACTA	GGGTGTCTGG CCCACAGACC	TCAGAGACAT AGTCTCTGTA	CAAGAAATAA GTTCTTTATT	CGCCGGAACA GCGGCCTTGT
2251	TTAGTGCAGG AATCACGTCC	CAGCTTCCAC GTCGAAGGTG	AGCAATAGCA TCGTTATCGT	TCCTGGTCAT AGGACCAGTA	CCAGCGGATA GGTCGCCTAT

ApaLI

~~~~~

Fig. 12 (cont.)

40/57

2301 GTTAATAATC AGCCCACTGA CACGTTGCGC GAGAAGATTG TGCACCGCCG  
CAATTATTAG TCGGGTGACT GTGCAACGCG CTCTTCTAAC ACGTGGCGGC

2351 CTTTACAGGC TTCGACGCCG CTTCGTTCTA CCATCGACAC GACCACGCTG  
GAAATGTCCG AAGCTGCGGC GAAGCAAGAT GGTAGCTGTG CTGGTGCGAC

2401 GCACCCAGTT GATCGGCGCG AGATTTAATC GCCGCGACAA TTTGCGACGG  
CGTGGGTCAA CTAGCCGCGC TCTAAATTAG CGGCGCTGTT AAACGCTGCC

2451 CGCGTGCAGG GCCAGACTGG AGGTGGCAAC GCCAATCAGC AACGACTGTT  
GCGCACGTCC CGGTCTGACC TCCACCGTTG CGGTAGTTCG TTGCTGACAA

2501 TGCCCGCCAG TTGTTGTGCC ACGCGGTTAG GAATGTAATT CAGCTCCGCC  
ACGGGCGGTC AACAAACAGG TGCGCCAATC CTTACATTAA GTCGAGGCGG

2551 ATCGCCGCTT CCACTTTTTTC CCGCGTTTTTC GCAGAAACGT GGCTGGCCTG  
TAGCGGCGAA GGTGAAAAAG GGCGCAAAAG CGTCTTTGCA CCGACCGGAC

2601 GTTCACCACG CGGGAAACGG TCTGATAAGA GACACCGGCA TACTCTGCGA  
CAAGTGGTGC GCCCTTTGCG AGACTATTCT CTGTGGCCGT ATGAGACGCT

2651 CATCGTATAA CGTTACTGGT TTCACATTCA CCACCCTGAA TTGACTCTCT  
GTAGCATATT GCAATGACCA AAGTGTAAGT GGTGGGACTT AACTGAGAGA

2701 TCCGGGCGCT ATCATGCCAT ACCGCGAAAG GTTTTGCGCC ATTCGATGCT  
AGGCCCCGCA TAGTACGGTA TGGCGCTTTC CAAAACGCGG TAAGCTACGA

2751 AGCCATGTGA GCAAAAGGCC AGCAAAAGGC CAGGAACCGT AAAAAGGCCG  
TCGGTACACT CGTTTTCCGG TCGTTTTCCG GTCCTTGCA TTTTTCGGC

2801 CGTTGCTGGC GTTTTTCCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA  
GCAACGACCG CAAAAAGGTA TCCGAGGCGG GGGGACTGCT CGTAGTGTTT

2851 AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC TATAAAGATA  
TTAGCTGCGA GTTCAGTCTC CACCGCTTTG GGCTGTCTTG ATATTCTAT

2901 CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC  
GGTCCGCAA GGGGGACCTT CGAGGGAGCA CGCGAGAGGA CAAGGCTGGG

2951 TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG  
ACGGCGAATG GCCTATGGAC AGGCGGAAAG AGGGAAGCCC TTCGCACCGC

3001 CTTTCTCATA GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTCTG  
GAAAGAGTAT CGAGTGCGAC ATCCATAGAG TCAAGCCACA TCCAGCAAGC

ApaLI

~~~~~

3051 CTCCAAGCTG GGCTGTGTGC ACGAACCCCC CGTTCAGCCC GACCGCTGCG  
GAGGTTTCGAC CCGACACACG TGCTTGGGGG GCAAGTCGGG CTGGCGACGC

3101 CCTTATCCGG TAACTATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA  
GGAATAGGCC ATTGATAGCA GAACTCAGGT TGGGCCATTG TGTGCTGAAT

Fig. 12 (cont.)

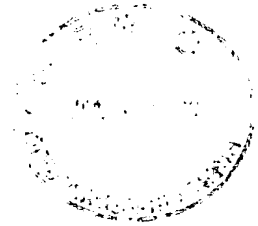


41/57

3151	TCGCCACTGG AGCGGTGACC	CAGCAGCCAC GTCGTCGGTG	TGGTAACAGG ACCATTGTCC	ATTAGCAGAG TAATCGTCTC	CGAGGTATGT GCTCCATACA
3201	AGGCGGTGCT TCCGCCACGA	ACAGAGTTCT TGTCTCAAGA	TGAAGTGGTG ACTTCACCAC	GCCTAACTAC CGGATTGATG	GGCTACACTA CCGATGTGAT
3251	GAAGAACAGT CTTCTTGTC	ATTTGGTATC TAAACCATAG	TGCGCTCTGC ACGCGAGACG	TGTAGCCAGT ACATCGGTCA	TACCTTCGGA ATGGAAGCCT
3301	AAAAGAGTTG TTTTCTCAAC	GTAGCTCTTG CATCGAGAAC	ATCCGGCAAA TAGGCCGTTT	CAAACCACCG GTTTGGTGCC	CTGGTAGCGG GACCATCGCC
3351	TGGTTTTTTT ACCAAAAAAA	GTTTGCAAGC CAAACGTTTC	AGCAGATTAC TCGTCTAATG	GCGCAGAAAA CGCGTCTTTT	AAAGGATCTC TTTCTAGAG
3401	AAGAAGATCC TTCTTCTAGG	TTTGATCTTT AAACTAGAAA	TCTACGGGGT AGATGCCCCA	CTGACGCTCA GACTGCGAGT	GTGGAACGAA CACCTTGCTT
3451	AACTCACGTT TTGAGTGCAA	AAGGGATTTT TTCCTAAAA	GGTCAGATCT CCAGTCTAGA	AGCACCAGGC TCGTGGTCCG	GTTTAAGGGC CAAATTCCCC
3501	ACCAATAACT TGTTATTGA	GCCTTAAAAA CGGAATTTTT	AATTACGCCC TTAATGCGGG	CGCCCTGCCA GCGGGACGGT	CTCATCGCAG GAGTAGCGTC
3551	TACTGTTGTA ATGACAACAT	ATTCATTAAG TAAGTAATTC	CATTCTGCCG GTAAGACGGC	ACATGGAAGC TGTACCTTCG	CATCACAAAC GTAGTGTGTT
3601	GGCATGATGA CCGTACTACT	ACCTGAATCG TGGACTTAGC	CCAGCGGCAT GGTCGCCGTA	CAGCACCTTG GTCGTGGAAC	TCGCCTTGCG AGCGGAACGC
3651	TATAATATTT ATATTATAAA	GCCCATAGTG CGGGTATCAC	AAAACGGGGG TTTTGCCCCC	CGAAGAAGTT GCTTCTTCAA	GTCCATATTG CAGGTATAAC
3701	GCTACGTTTA CGATGCAAAT	AATCAAAACT TTAGTTTTGA	GGTGAAACTC CCACTTTGAG	ACCCAGGGAT TGGGTCCCTA	TGGCTGAGAC ACCGACTCTG
3751	GAAAAACATA CTTTTTGTAT	TTCTCAATAA AAGAGTTATT	ACCCTTTAGG TGGGAAATCC	GAAATAGGCC CTTTATCCGG	AGGTTTTTCAC TCCAAAAGTG
3801	CGTAACACGC GCATTGTGCG	CACATCTTGC GTGTAGAACG	GAATATATGT CTTATATACA	GTAGAAACTG CATCTTTGAC	CCGGAAATCG GGCCTTTAGC
3851	TCGTGGTATT AGCACCATAA	CACTCCAGAG GTGAGGTCTC	CGATGAAAAC GCTACTTTTG	GTTTCAGTTT CAAAGTCAAA	GCTCATGGAA CGAGTACCTT
3901	AACGGTGTA TTGCCACATT	CAAGGGTGAA GTTCCCACTT	CACTATCCCA GTGATAGGGT	TATCACCAGC ATAGTGGTCG	TCACCGTCTT AGTGGCAGAA
3951	TCATTGCCAT AGTAACGGTA	ACGGAACCTC TGCCTTGAGG	GGGTGAGCAT CCCACTCGTA	TCATCAGGCG AGTAGTCCGC	GGCAAGAATG CCGTTCTTAC

Fig. 12 (cont.)

42/57



4001 TGAATAAAGG CCGGATAAAA CTTGTGCTTA TTTTCTTTA CGGTCTTTAA  
 ACTTATTTCC GGCCTATTTT GAACACGAAT AAAAAGAAAT GCCAGAAATT  
 4051 AAAGGCCGTA ATATCCAGCT GAACGGTCTG GTTATAGGTA CATTGAGCAA  
 TTTCGGGCAT TATAGGTCGA CTTGCCAGAC CAATATCCAT GTAACCTCGTT  
 4101 CTGACTGAAA TGCCTCAAAA TGTTCCTTAC GATGCCATTG GGATATATCA  
 GACTGACTTT ACGGAGTTTT ACAAGAAATG CTACGGTAAC CCTATATAGT  
 4151 ACGGTGGTAT ATCCAGTGAT TTTTTCTCC ATTTTAGCTT CCTTAGCTCC  
 TGCCACCATA TAGGTCACTA AAAAAGAGG TAAAATCGAA GGAATCGAGG  
 4201 TGAAAATCTC GATAACTCAA AAAATACGCC CGGTAGTGAT CTTATTTTCAT  
 ACTTTTAGAG CTATTGAGTT TTTTATGCGG GCCATCACTA GAATAAAGTA  
 4251 TATGGTGAAA GTTGGAACTT CACCCGACGT CTAATGTGAG TTAGCTCACT  
 ATACCACTTT CAACCTTGGA GTGGGCTGCA GATTACACTC AATCGAGTGA  
 4301 CATTAGGCAC CCCAGGCTTT ACACTTTATG CTTCCGGCTC GTATGTTGTG  
 GTAATCCGTG GGTCCGAAA TGTGAAATAC GAAGGCCGAG CATAACAAC  
 M13 Reverse primer 100.0%  
 =====  
 4351 TGGAATTGTG AGCGGATAAC AATTTACAC AGGAAACAGC TATGACCATG  
 ACCTTAACAC TCGCCTATTG TTAAAGTGTG TCCTTTGTG ATACTGGTAC  
 4401 ATTACGAATT  
 TAATGCTTAA

Fig. 12 (cont.)

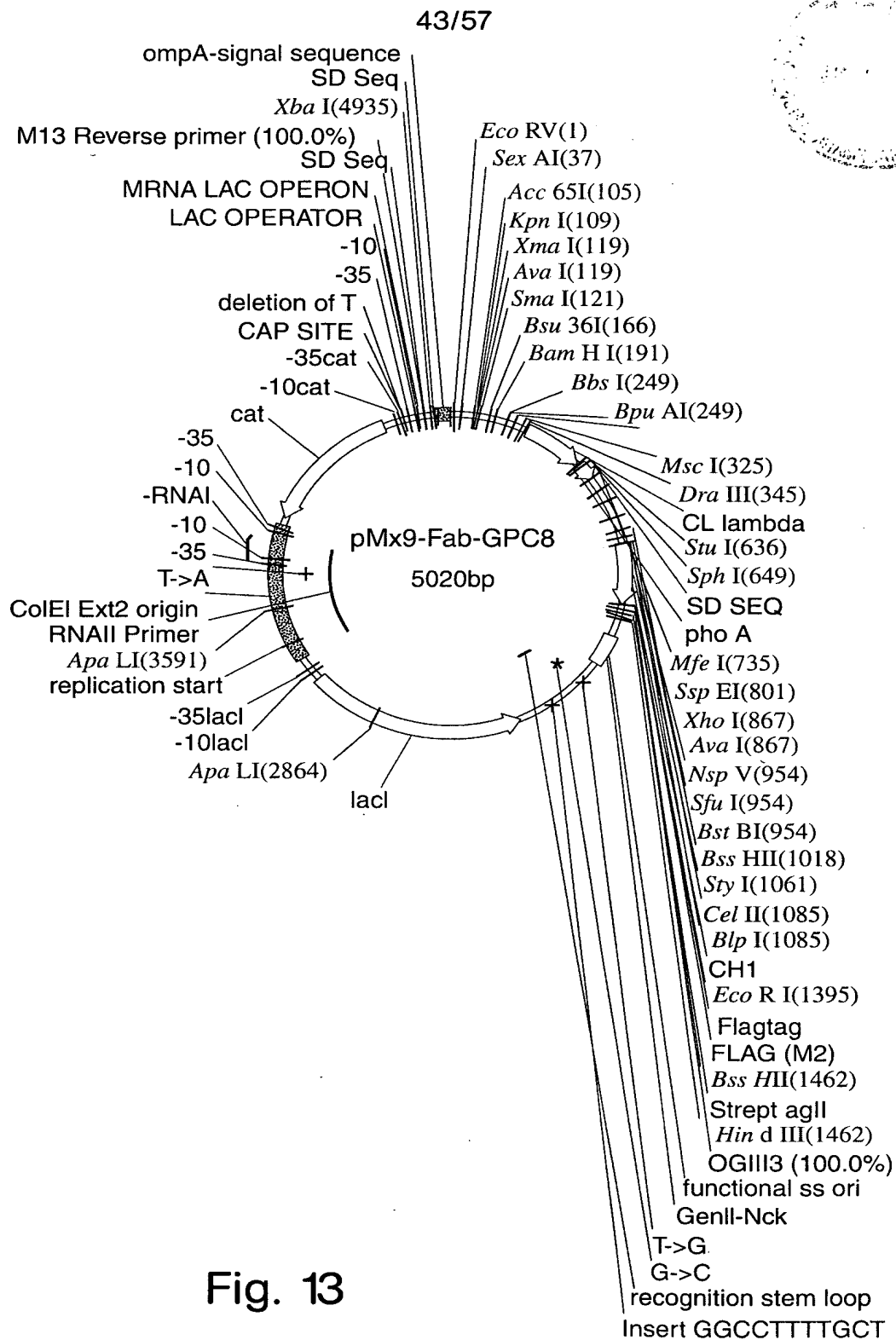


Fig. 13

44/57

EcoRV  
 ~~~  
 1 ATCGTGCTGA CCCAGCCGCC TTCAGTGAGT GGCGCACCAG GTCAGCGTGT  
 TAGCACGACT GGGTCGGCGG AAGTCACTCA CCGCGTGGTC CAGTCGCACA  
 51 GACCATCTCG TGTAGCGGCA GCAGCAGCAA CATTGGCAGC AACTATGTGA  
 CTGGTAGAGC ACATCGCCGT CGTCGTCGTT GTAACCGTCG TTGATACACT

XmaI  
 ~~~~~  
 KpnI  
 ~~~~~  
 SmaI  
 ~~~~~  
 Acc65I  
 ~~~~~  
 AvaI  
 ~~~~~

101 GCTGGTACCA GCAGTTGCCC GGGACGGCGC CGAAACTGCT GATTTATGAT  
 CGACCATGGT CGTCAACGGG CCCTGCCGCG GCTTTGACGA CTAAATACTA

Bsu36I  
 ~~~~~  
 151 AACAAACCAGC GTCCCTCAGG CGTGCCGGAT CGTTTTAGCG GATCCAAAAG  
 TTGTTGGTCG CAGGGAGTCC GCACGGCCTA GCAAATCGC CTAGGTTTTCT

BamHI  
 ~~~~~  
 BpuAI  
 ~~~~~  
 BbsI  
 ~~~~~

201 CGGCACCAGC GCGAGCCTTG CGATTACGGG CCTGCAAAGC GAAGACGAAG  
 GCCGTGGTCG CGCTCGGAAC GCTAATGCCC GGACGTTTCG CTTCTGCTTC

Bsu36I  
 ~~~~~

251 CGGATTATTA TTGCCAGAGC TATGACATGC CTCAGGCTGT GTTTGGCGGC  
 GCCTAATAAT AACGGTCTCG ATACTGTACG GAGTCCGACA CAAACCGCCG

MscI  
 ~~~~~  
 DraIII  
 ~~~~~

301 GGCACGAAGT TTAACCGTTC TTGGCCAGCC GAAAGCCGCA CCGAGTGTGA  
 CCGTGCTTCA AATTGGCAAG AACC GGTCGG CTTTCGGCGT GGCTCACACT

351 CGCTGTTTCC GCCGAGCAGC GAAGAATTGC AGGCGAACAA AGCGACCTTG  
 GCGACAAAGG CGGCTCGTCG CTTCTTAACG TCCGCTTGTT TCGCTGGGAC

401 GTGTGCCTGA TTAGCGACTT TTATCCGGGA GCCGTGACAG TGGCCTGGAA  
 CACACGGACT AATCGCTGAA AATAGGCCCT CGGCACTGTC ACCGGACCTT

451 GGCAGATAGC AGCCCCGTCA AGGCGGGAGT GGAGACCACC ACACCCTCCA  
 CCGTCTATCG TCGGGGCAGT TCCGCCCTCA CCTCTGGTGG TGTGGGAGGT

501 AACAAAGCAA CAACAAGTAC GCGGCCAGCA GCTATCTGAG CCTGACGCCT  
 TTGTTTCGTT GTTGTTTCATG CGCCGGTCGT CGATAGACTC GGACTGCGGA

Fig. 13 (cont.)

45/57

551 GAGCAGTGGA AGTCCCACAG AAGCTACAGC TGCCAGGTCA CGCATGAGGG  
CTCGTCACCT TCAGGGTGTC TTCGATGTCG ACGGTCCAGT GCGTACTGCC

StuI                      SphI  
~~~~~                      ~~~~~

601 GAGCACCGTG GAAAAAACCG TTGCGCCGAC TGAGGCCTGA TAAGCATGCG  
CTCGTGGCAC CTTTTTTGGC AACGCGGCTG ACTCCGGACT ATTCGTACGC

651 TAGGAGAAAA TAAAATGAAA CAAAGCACTA TTGCACTGGC ACTCTTACCG  
ATCCTCTTTT ATTTTACTTT GTTTCGTGAT AACGTGACCG TGAGAATGGC

MfeI  
~~~~~

701 TTGCTCTTCA CCCCTGTTAC CAAAGCCCAG GTGCAATTGA AAGAAAGCGG  
AACGAGAAGT GGGGACAATG GTTTCGGGTC CACGTAACT TTCTTTCGCC

BspEI  
~

751 CCCGGCCCTG GTGAAACCGA CCCAAACCCT GACCCTGACC TGTACCTTTT  
GGGCCGGGAC CACTTTGGCT GGGTTTGGGA CTGGGACTGG ACATGGAAAA

BspEI  
~~~~~

801 CCGGATTTAG CCTGTCCACG TCTGGCGTTG GCGTGGGCTG GATTTCGCCAG  
GGCCTAAATC GGACAGGTGC AGACCGCAAC CGCACCCGAC CTAAGCGGTC

XhoI  
~~~~~  
AvaI  
~~~~~

851 CCGCCTGGGA AAGCCCTCGA GTGGCTGGCT CTGATTGATT GGGATGATGA  
GGCGGACCCT TTCGGGAGCT CACCGACCGA GACTAACTAA CCCTACTACT

901 TAAGTATTAT AGCACCAGCC TGAAAACGCG TCTGACCATT AGCAAAGATA  
ATTCATAATA TCGTGGTCGG ACTTTTGCGC AGACTGGTAA TCGTTTCTAT

BstBI  
~~~~~  
SfuI  
~~~~~  
NspV  
~~~~~

951 CTTTCGAAAA TCAGGTGGTG CTGACTATGA CCAACATGGA CCCGGTGGAT  
GAAGCTTTTT AGTCCACCAC GACTGATACT GGTGTACCT GGGCCACCTA

BssHII  
~~~~~

1001 ACGGCCACCT ATTATTGCGC GCGTTCTCCT CGTTATCGTG GTGCTTTTGA  
TGCCGGTGGA TAATAACGCG CGCAAGAGGA GCAATAGCAC CACGAAAACT

BlnI

Fig. 13 (cont.)

46/57

StyI  
~~~~~

~~~~~  
CelIII  
~~~~~

1051 TTATTGGGGC CAAGGCACCC TGGTGACGGT TAGCTCAGCG TCGACCAAAG  
AATAACCCCG GTTCCGTGGG ACCACTGCCA ATCGAGTCGC AGCTGGTTTC

1101 GTCCAAGCGT GTTTCGCTG GCTCCGAGCA GCAAAAGCAC CAGCGGCGGC  
CAGGTTCGCA CAAAGGCGAC CGAGGCTCGT CGTTTTTCGTG GTCGCCGCCG

1151 ACGGCTGCCC TGGGCTGCCT GGTTAAAGAT TATTTCCCGG AACCAGTCAC  
TGCCGACGGG ACCCGACGGA CCAATTTCTA ATAAAGGGCC TTGGTCAGTG

1201 CGTGAGCTGG AACAGCGGGG CGCTGACCAG CGGCGTGCAT ACCTTTCCGG  
GCACTCGACC TTGTCGCCCC GCGACTGGTC GCCGCACGTA TGGAAAGGCC

1251 CGGTGCTGCA AAGCAGCGGC CTGTATAGCC TGAGCAGCGT TGTGACCGTG  
GCCACGACGT TTCGTCGCCG GACATATCGG ACTCGTCGCA ACACTGGCAC

1301 CCGAGCAGCA GCTTAGGCAC TCAGACCTAT ATTTGCAACG TGAACCATAA  
GGCTCGTCGT CGAATCCGTG AGTCTGGATA TAAACGTTGC ACTTGGTATT

EcoRI  
~~~~~

1351 ACCGAGCAAC ACCAAAGTGG ATAAAAAAGT GGAACCGAAA AGCGAATTCG  
TGGCTCGTTG TGGTTTCACC TATTTTTTCA CCTTGGCTTT TCGCTTAAGC

BssHII  
~~~~~

1401 ACTATAAAGA TGACGATGAC AAAGGCGCGC CGTGGAGCCA CCCGCAGTTT  
TGATATTTCT ACTGCTACTG TTTCCGCGCG GCACCTCGGT GGGCGTCAAA

HindIII  
~~~~~

1451 GAAAAATGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG  
CTTTTTACTA TTCGAAGTGG ACACCTTCACT TTTTACCGCG TCTAACACGC

OGIII3 100.0%  
=====

1501 ACATTTTTTTT TGTCTGCCGT TTAATTAAAG GGGGGGGGGG GCCGGCCTGG  
TGTAACAAAAA ACAGACGGCA AATTAATTTT CCCCCCCCCC CGGCCGGACC

1551 GGGGGGGTGT ACATGAAATT GTAAACGTTA ATATTTTGTT AAAATTCGCG  
CCCCCCCACA TGTACTTTAA CATTTGCAAT TATAAAACAA TTTTAAGCGC

1601 TTAAATTTTTT GTTAAATCAG CTCATTTTTT AACCAATAGG CCGAAATCGG  
AATTTAAAAA CAATTTAGTC GAGTAAAAAA TTGGTTATCC GGCTTTAGCC

1651 CAAAATCCCT TATAAATCAA AAGAATAGAC CGAGATAGGG TTGAGTGTTG  
GTTTTAGGGA ATATTTAGTT TTCTTATCTG GCTCTATCCC AACTCACAAC

1701 TTCCAGTTTG GAACAAGAGT CCACTATTAA AGAACGTGGA CTCCAACGTC  
AAGGTCAAAC CTTGTTCTCA GGTGATAATT TCTTGACCT GAGGTTGCAG

Fig. 13 (cont.)

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|      |                          |                           |                           |                           |                           |
|------|--------------------------|---------------------------|---------------------------|---------------------------|---------------------------|
| 1751 | AAAGGGCGAA<br>TTTCCCCTT  | AAACCGTCTA<br>TTTGGCAGAT  | TCAGGGCGAT<br>AGTCCCCTA   | GGCCCACTAC<br>CCGGGTGATG  | GAGAACCATC<br>CTCTTGGTAG  |
| 1801 | ACCCTAATCA<br>TGGGATTAGT | AGTTTTTTTGG<br>TCAAAAAACC | GGTCGAGGTG<br>CCAGCTCCAC  | CCGTAAAGCA<br>GGCATTTTCGT | CTAAATCGGA<br>GATTTAGCCT  |
| 1851 | ACCCTAAAGG<br>TGGGATTTCC | GAGCCCCCGA<br>CTCGGGGGCT  | TTTAGAGCTT<br>AAATCTCGAA  | GACGGGGAAA<br>CTGCCCCCTT  | GCCGGCGAAC<br>CGGCCGCTTG  |
| 1901 | GTGGCGAGAA<br>CACCCTCTT  | AGGAAGGGAA<br>TCCTTCCCTT  | GAAAGCGAAA<br>CTTTCGCTTT  | GGAGCGGGCG<br>CCTCGCCCGC  | CTAGGGCGCT<br>GATCCCGCGA  |
| 1951 | GGCAAGTGTA<br>CCGTTACAT  | GCGGTCACGC<br>CGCCAGTGCG  | TGCGCGTAAC<br>ACGCGCATTG  | CACCACACCC<br>GTGGTGTGGG  | GCCGCGCTTA<br>CGGCGCGAAT  |
| 2001 | ATGCGCCGCT<br>TACGCGGCGA | ACAGGGCGCG<br>TGTCCCCTCGC | TGCTAGACTA<br>ACGATCTGAT  | GTGTTTAAAC<br>CACAAATTTG  | CGGACCGGGG<br>GCCTGGCCCC  |
| 2051 | GGGGGCTTAA<br>CCCCGAATT  | GTGGGCTGCA<br>CACCCGACGT  | AAACAAAACG<br>TTTGTTTTGC  | GCCTCCTGTC<br>CGGAGGACAG  | AGGAAGCCGC<br>TCCTTCGGCG  |
| 2101 | TTTTATCGGG<br>AAAATAGCCC | TAGCCTCACT<br>ATCGGAGTGA  | GCCCCGCTTTC<br>CGGGCGAAAG | CAGTCGGGAA<br>GTCAGCCCTT  | ACCTGTTCGTG<br>TGGACAGCAC |
| 2151 | CCAGCTGCAT<br>GGTCGACGTA | CAGTGAATCG<br>GTCACCTAGC  | GCCAACGCGC<br>CGGTTGCGCG  | GGGGAGAGGC<br>CCCCTCTCCG  | GGTTTGCGTA<br>CCAAACGCAT  |
| 2201 | TTGGGAGCCA<br>AACCCTCGGT | GGGTGGTTTT<br>CCCACCAAAA  | TCTTTTCACC<br>AGAAAAGTGG  | AGTGAGACGG<br>TCACTCTGCC  | GCAACAGCTG<br>CGTTGTGCAC  |
| 2251 | ATTGCCCTTC<br>TAACGGGAAG | ACCGCCTGGC<br>TGGCGGACCG  | CCTGAGAGAG<br>GGACTCTCTC  | TTGCAGCAAG<br>AACGTCGTTC  | CGGTCCACGC<br>GCCAGGTGCG  |
| 2301 | TGGTTTGCCC<br>ACCAAACGGG | CAGCAGGCGA<br>GTCGTCCGCT  | AAATCCTGTT<br>TTTAGGACAA  | TGATGGTGGT<br>ACTACCACCA  | CAGCGGCGGG<br>GTCGCCGCCC  |
| 2351 | ATATAACATG<br>TATATTGTAC | AGCTGTCCCTC<br>TCGACAGGAG | GGTATCGTCG<br>CCATAGCAGC  | TATCCCCTA<br>ATAGGGTGAT   | CCGAGATGTC<br>GGCTCTACAG  |
| 2401 | CGCACCAACG<br>GCGTGGTTGC | CGCAGCCCCG<br>GCGTCGGGCC  | ACTCGGTAAT<br>TGAGCCATTA  | GGCAGCATT<br>CCGTGCGTAA   | GCGCCAGCG<br>CGCGGGTCGC   |
| 2451 | CCATCTGATC<br>GGTAGACTAG | GTTGGCAACC<br>CAACCGTTGG  | AGCATCGCAG<br>TCGTAGCGTC  | TGGGAACGAT<br>ACCCTTGCTA  | GCCCTCATTC<br>CGGGAGTAAG  |
| 2501 | AGCATTTGCA<br>TCGTAAACGT | TGGTTTGTG<br>ACCAAACAAC   | AAAACCGGAC<br>TTTTGGCCTG  | ATGGCACTCC<br>TACCGTGAGG  | AGTCGCCTTC<br>TCAGCGGAAG  |
| 2551 | CCGTTCCGCT<br>GGCAAGGCGA | ATCGGCTGAA<br>TAGCCGACTT  | TTTGATTGCG<br>AAACTAACGC  | AGTGAGATAT<br>TCACTCTATA  | TTATGCCAGC<br>AATACGGTCG  |

Fig. 13 (cont.)

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|      |                          |                          |                          |                           |                          |
|------|--------------------------|--------------------------|--------------------------|---------------------------|--------------------------|
| 2601 | CAGCCAGACG<br>GTCGGTCTGC | CAGACGCGCC<br>GTCTGCGCGG | GAGACAGAAC<br>CTCTGTCTTG | TTAATGGGCG<br>AATTACCCGG  | AGCTAACAGC<br>TCGATTGTCG |
| 2651 | GCGATTTGCT<br>CGCTAAACGA | GGTGGCCCAA<br>CCACCGGGTT | TGCGACCAGA<br>ACGCTGGTCT | TGCTCCACGC<br>ACGAGGTGCG  | CCAGTCGCGT<br>GGTCAGCGCA |
| 2701 | ACCGTCCTCA<br>TGGCAGGAGT | TGGGAGAAAA<br>ACCCTCTTTT | TAATACTGTT<br>ATTATGACAA | GATGGGTGTC<br>CTACCCACAG  | TGGTCAGAGA<br>ACCAGTCTCT |
| 2751 | CATCAAGAAA<br>GTAGTTCTTT | TAACGCCGGA<br>ATTGCGGCCT | ACATTAGTGC<br>TGTAATCACG | AGGCAGCTTC<br>TCCGTCTGAAG | CACAGCAATA<br>GTGTCGTTAT |
| 2801 | GCATCCTGGT<br>CGTAGGACCA | CATCCAGCGG<br>GTAGGTCGCC | ATAGTTAATA<br>TATCAATTAT | ATCAGCCAC<br>TAGTCGGGTG   | TGACACGTTG<br>ACTGTGCAAC |

## ApaLI

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2851	CGCGAGAAGA GCGCTCTTCT	TTGTGCACCG AACACGTGGC	CCGCTTTTACA GGCGAAATGT	GGCTTCGACG CCGAAGCTGC	CCGCTTCGTT GGCGAAGCAA
2901	CTACCATCGA GATGGTAGCT	CACGACCACG GTGCTGGTGC	CTGGCACCCA GACCGTGGGT	GTTGATCGGC CAACTAGCCG	GCGAGATTTA CGCTCTAAAT
2951	ATCGCCGCGA TAGCGGCGCT	CAATTTGCGA GTTAAACGCT	CGGCGCGTGC GCCGCGCACG	AGGGCCAGAC TCCCGGTCTG	TGGAGGTGGC ACCTCCACCG
3001	AACGCCAATC TTGCGGTTAG	AGCAACGACT TCGTTGCTGA	GTTTGCCCGC CAAACGGGCG	CAGTTGTTGT GTCAACAACA	GCCACGCGGT CGGTGCGCCA
3051	TAGGAATGTA ATCCTTACAT	ATTCAGCTCC TAAGTCGAGG	GCCATCGCCG CGGTAGCGGC	CTTCCACTTT GAAGGTGAAA	TTCCCGCGTT AAGGGCGCAA
3101	TTCGCAGAAA AAGCGTCTTT	CGTGGCTGGC GCACCGACCG	CTGGTTCACC GACCAAGTGG	ACGCGGGAAA TGCGCCCTTT	CGGTCTGATA GCCAGACTAT
3151	AGAGACACCG TCTCTGTGGC	GCATACTCTG CGTATGAGAC	CGACATCGTA GCTGTAGCAT	TAACGTTACT ATTGCAATGA	GGTTTCACAT CCAAAGTGTA
3201	TCACCACCCT AGTGGTGGGA	GAATTGACTC CTTAAGTGAG	TCTTCCGGGC AGAAGGCCCG	GCTATCATGC CGATAGTACG	CATACCGCGA GTATGGCGCT
3251	AAGGTTTTGC TTCCAAAACG	GCCATTCGAT CGGTAAGCTA	GCTAGCCATG CGATCGGTAC	TGAGCAAAAG ACTCGTTTTT	GCCAGCAAAA CGGTGCTTTT
3301	GGCCAGGAAC CCGGTCCTTG	CGTAAAAAGG GCATTTTTC	CCGCGTTGCT GGCGCAACGA	GGCGTTTTTC CCGCAAAAAG	CATAGGCTCC GTATCCGAGG
3351	GCCCCCCTGA CGGGGGGACT	CGAGCATCAC GCTCGTAGTG	AAAAATCGAC TTTTTAGCTG	GCTCAAGTCA CGAGTTCAGT	GAGGTGGCGA CTCCACCGCT
3401	AACCCGACAG	GACTATAAAG	ATACCAGGCG	TTTCCCCCTG	GAAGCTCCCT

Fig. 13 (cont.)



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	TTGGGCTGTC	CTGATATTTT	TATGGTCCGC	AAAGGGGGAC	CTTCGAGGGA
3451	CGTGCGCTCT GCACGCGAGA	CCTGTTCCGA GGACAAGGCT	CCCTGCCGCT GGGACGGCGA	TACCGGATAC ATGGCCTATG	CTGTCCGCCT GACAGGCGGA
3501	TTCTCCCTTC AAGAGGGAAG	GGGAAGCGTG CCCTTCGCAC	GCGCTTTTCTC CGCGAAAAGAG	ATAGCTCACG TATCGAGTGC	CTGTAGGTAT GACATCCATA
				~~~~~	
3551	CTCAGTTCGG GAGTCAAGCC	TGTAGGTCGT ACATCCAGCA	TCGCTCCAAG AGCGAGGTTT	CTGGGCTGTG GACCCGACAC	TGCACGAACC ACGTGCTTGG
3601	CCCCGTTTCA GGGGCAAGTC	CCCGACCGCT GGGCTGGCGA	GCGCCTTATC CGCGGAATAG	CGGTAACAT GCCATTGATA	CGTCTTGAGT GCAGAACTCA
3651	CCAACCCGGT GGTTGGGCCA	AAGACACGAC TTCTGTGCTG	TTATCGCCAC AATAGCGGTG	TGGCAGCAGC ACCGTCGTCT	CACTGGTAAC GTGACCATTG
3701	AGGATTAGCA TCCTAATCGT	GAGCGAGGTA CTCGCTCCAT	TGTAGGCGGT ACATCCGCCA	GCTACAGAGT CGATGTCTCA	TCTTGAAGTG AGAACTTCAC
3751	GTGGCCTAAC CACCGGATTG	TACGGCTACA ATGCCGATGT	CTAGAAGAAC GATCTTCTTG	AGTATTTGGT TCATAAACCA	ATCTGCGCTC TAGACGCGAG
3801	TGCTGTAGCC ACGACATCGG	AGTTACCTTC TCAATGGAAG	GGAAAAAGAG CCTTTTTTCTC	TTGGTAGCTC AACCATCGAG	TTGATCCGGC AACTAGGCCG
3851	AAACAAACCA TTTGTTTGGT	CCGCTGGTAG GGCGACCATC	CGGTGGTTTT GCCACCAAAA	TTTGTTTGCA AAACAAACGT	AGCAGCAGAT TCGTCTGCTA
3901	TACGCGCAGA ATGCGCGTCT	AAAAAAGGAT TTTTTTCCTA	CTCAAGAAGA GAGTTCTTCT	TCCTTTGATC AGGAAACTAG	TTTTCTACGG AAAAGATGCC
3951	GGTCTGACGC CCAGACTGCG	TCAGTGGAAC AGTCACCTTG	GAAAACTCAC CTTTTGAGTG	GTTAAGGGAT CAATTCCCTA	TTTGGTGAGA AAACCAGTCT
4001	TCTAGCACCA AGATCGTGGT	GGCGTTTAA CCGCAAATTC	GGCACCAATA CCGTGGTTAT	ACTGCCTTAA TGACGGAATT	AAAAATTACG TTTTTAATGC
4051	CCCCGCCCTG GGGGCGGGAC	CCACTCATCG GGTGAGTAGC	CAGTACTGTT GTCATGACAA	GTAATTCATT CATTAAGTAA	AAGCATTCTG TTCGTAAGAC
4101	CCGACATGGA GGCTGTACCT	AGCCATCACA TCGGTAGTGT	AACGGCATGA TTGCCGTACT	TGAACCTGAA ACTTGGAATT	TCGCCAGCGG AGCGGTCGCC
4151	CATCAGCACC GTAGTCGTGG	TTGTCGCCTT AACAGCGGAA	GCGTATAATA CGCATATTAT	TTTGCCCAT AAACGGGTAT	GTGAAAACGG CACTTTTGCC
4201	GGGCGAAGAA CCCCGCTTCTT	GTTGTCCATA CAACAGGTAT	TTGGCTACGT AACCGATGCA	TTAAATCAAA AATTTAGTTT	ACTGGTGAAA TGACCACTTT

Fig. 13 (cont.)

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4251 CTCACCCAGG GATTGGCTGA GACGAAAAAC ATATTCTCAA TAAACCCTTT  
 GAGTGGGTCC CTAACCGACT CTGCTTTTTG TATAAGAGTT ATTTGGGAAA  
 4301 AGGGAAATAG GCCAGGTTTT CACCGTAACA CGCCACATCT TGCGAATATA  
 TCCCTTTATC CGGTCCAAAA GTGGCATTGT GCGGTGTAGA ACGCTTATAT  
 4351 TGTGTAGAAA CTGCCGGAAG TCGTCGTGGT ATTCACTCCA GAGCGATGAA  
 ACACATCTTT GACGGCCTTT AGCAGCACCA TAAGTGAGGT CTCGCTACTT  
 4401 AACGTTTCAG TTTGCTCATG GAAAACGGTG TAACAAGGGT GAACACTATC  
 TTGCAAAGTC AAACGAGTAC CTTTTGCCAC ATTGTTCCCA CTTGTGATAG  
 4451 CCATATCACC AGCTCACCGT CTTTCATTGC CATACGGAAC TCCGGGTGAG  
 GGTATAGTGG TCGAGTGGCA GAAAGTAACG GTATGCCTTG AGGCCCACTC  
 4501 CATTTCATCAG GCGGGCAAGA ATGTGAATAA AGGCCGGATA AAACCTGTGC  
 GTAAGTAGTC CGCCCGTTCT TACACTTATT TCCGGCCTAT TTTGAACACG  
 4551 TTATTTTTCT TTACGGTCTT TAAAAGGCC GTAATATCCA GCTGAACGGT  
 AATAAAAAGA AATGCCAGAA ATTTTTCCGG CATTATAGGT CGACTTGCCA  
 4601 CTGGTTATAG GTACATTGAG CAACTGACTG AAATGCCTCA AAATGTTCTT  
 GACCAATATC CATGTAACCTC GTTGACTGAC TTTACGGAGT TTTACAAGAA  
 4651 TACGATGCCA TTGGGATATA TCAACGGTGG TATATCCAGT GATTTTTTTC  
 ATGCTACGGT AACCCATATAT AGTTGCCACC ATATAGGTCA CTAAAAAAG  
 4701 TCCATTTTAG CTTCTTAGC TCCTGAAAAT CTCGATAACT CAAAAAATAC  
 AGGTAAAATC GAAGGAATCG AGGACTTTTA GAGCTATTGA GTTTTTTATG  
 4751 GCCCGGTAGT GATCTTATTT CATTATGGTG AAAGTTGGAA CCTCACCCGA  
 CGGGCCATCA CTAGAATAAA GTAATACCAC TTTCAACCTT GGAGTGGGCT  
 4801 CGTCTAATGT GAGTTAGCTC ACTCATTAGG CACCCCAGGC TTTACACTTT  
 GCAGATTACA CTCAATCGAG TGAGTAATCC GTGGGGTCCG AAATGTGAAA  
 4851 ATGCTTCCGG CTCGTATGTT GTGTGGAATT GTGAGCGGAT AACAAATTTCA  
 TACGAAGGCC GAGCATACAA CACACCTTAA CACTCGCCTA TTGTTAAAGT  
  
 M13 Reverse primer 100.0% XbaI  
 =====  
 4901 CACAGGAAAC AGCTATGACC ATGATTACGA ATTTCTAGAT AACGAGGGCA  
 GTGTCCCTTTG TCGATACTGG TACTAATGCT TAAAGATCTA TTGCTCCCGT  
 4951 AAAAAATGAAA AAGACAGCTA TCGCGATTGC AGTGGCACTG GCTGGTTTTCG  
 TTTTTACTTT TTCTGTCTGAT AGCGCTAACG TCACCGTGAC CGACCAAAGC  
  
 EcoRV  
 ~~~~  
 5001 CTACCGTAGC GCAGGCCGAT  
 GATGGCATCG CGTCCGGCTA

Fig. 13 (cont.)

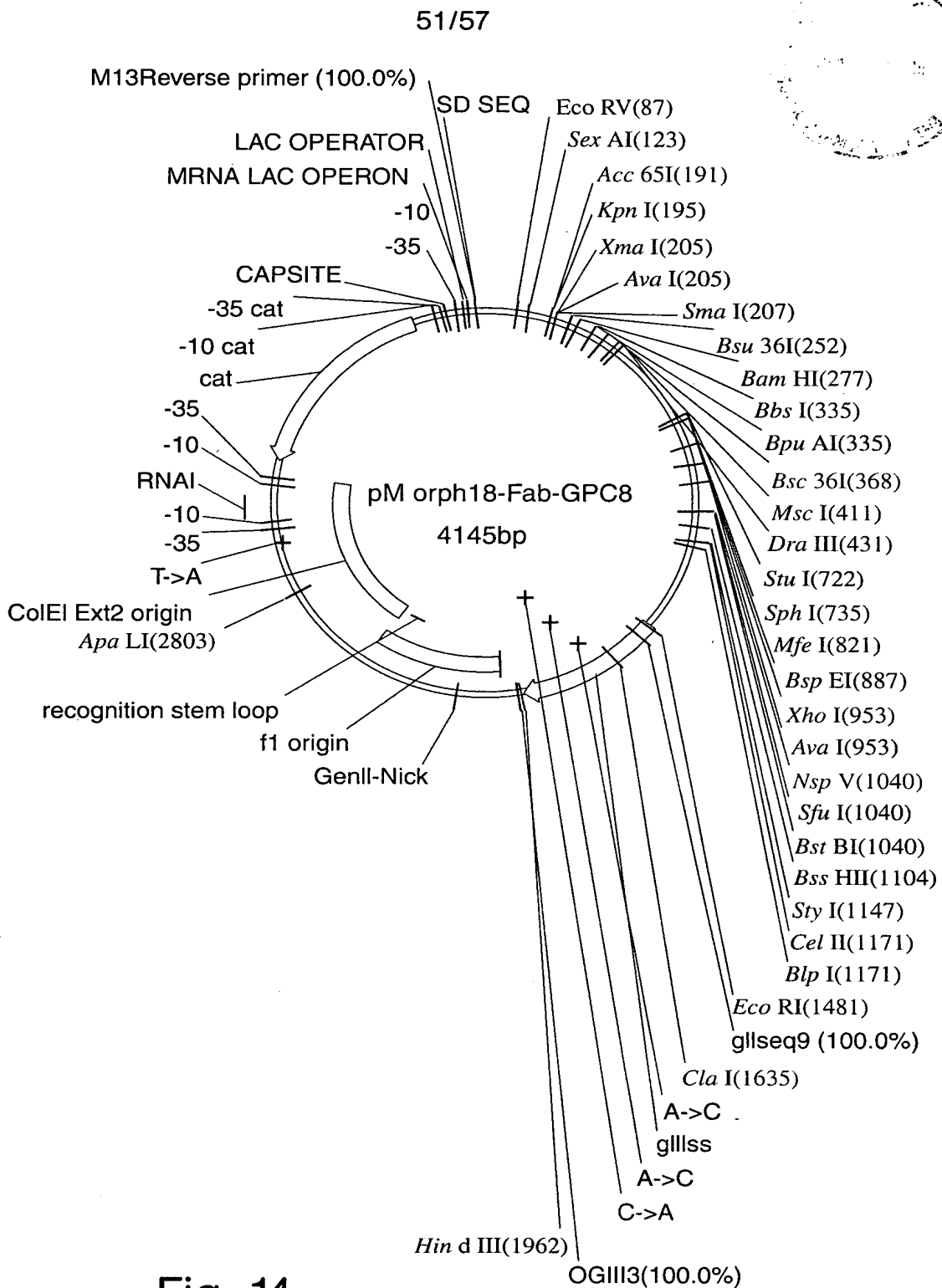


Fig. 14

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1 TCAGATAACG AGGGCAAAAA ATGAAAAAGA CAGCTATCGC GATTGCAGTG  
AGTCTATTGC TCCCGTTTTT TACTTTTTTCT GTCGATAGCG CTAACGTCAC

EcoRV  
~~~~~

51 GCACTGGCTG GTTTCGCTAC CGTAGCGCAG GCCGATATCG TGCTGACCCA  
CGTGACCGAC CAAAGCGATG GCATCGCGTC CGGCTATAGC ACGACTGGGT

SexAI  
~~~~~

101 GCCGCCTTCA GTGAGTGGCG CACCAGGTCA GCGTGTGACC ATCTCGTGTA  
CGGCGGAAGT CACTCACC GC TGGTCCAGT CGCACACTGG TAGAGCACAT

KpnI  
~~~~~  
Acc65I  
~~~~~

151 GCGGCAGCAG CAGCAACATT GGCAGCAACT ATGTGAGCTG GTACCAGCAG  
CGCCGTCGTC GTCGTTGTAA CCGTCGTTGA TACACTCGAC CATGGTCGTC

XmaI  
~~~~~  
SmaI  
~~~~~  
AvaI  
~~~~~

Bsu36I  
~

201 TTGCCCCGGA CGGCGCCGAA ACTGCTGATT TATGATAACA ACCAGCGTCC  
AACGGGCCCT GCCGCGGCTT TGACGACTAA ATACTATTGT TGGTCGCAGG

Bsu36I  
~~~~~

BamHI  
~~~~~

251 CTCAGGCGTG CCGGATCGTT TTAGCGGATC CAAAAGCGGC ACCAGCGCGA  
GAGTCCGCAC GGCCTAGCAA AATCGCCTAG GTTTTCGCCG TGGTCGCGCT

BpuAI  
~~~~~  
BbsI  
~~~~~

301 GCCTTGCGAT TACGGGCCTG CAAAGCGAAG ACGAAGCGGA TTATTATTGC  
CGGAACGCTA ATGCCCGGAC GTTTCGCTTC TGCTTCGCCT AATAATAACG

Bsu36I  
~~~~~

351 CAGAGCTATG ACATGCCTCA GGCTGTGTTT GCGGCGGCA CGAAGTTTAA  
GTCTCGATAC TGTACGGAGT CCGACACAAA CCGCCGCCGT GCTTCAAATT

MscI  
~~~~~

DraIII  
~~~~~

401 CCGTTCTTGG CCAGCCGAAA GCCGCACCGA GTGTGACGCT GTTTCGCCG  
GGCAAGAACC GGTCGGCTTT CGGCGTGGCT CACACTGCGA CAAAGGCGGC

451 AGCAGCGAAG AATTGCAGGC GAACAAAGCG ACCCTGGTGT GCCTGATTAG  
TCGTCGCTTC TTAACGTCCG CTTGTTTCGC TGGGACCACA CGGACTAATC

501 CGACTTTTAT CCGGGAGCCG TGACAGTGGC CTGGAAGGCA GATAGCAGCC

Fig. 14 (cont.)

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|      |            |            |            |            |             |
|------|------------|------------|------------|------------|-------------|
|      | GCTGAAAATA | GGCCCTCGGC | ACTGTCACCG | GACCTTCCGT | CTATCGTCGG  |
| 551  | CCGTCAAGGC | GGGAGTGGAG | ACCACCACAC | CCTCCAAACA | AAGCAACAAC  |
|      | GGCAGTTCCG | CCCTCACCTC | TGGTGGTGTG | GGAGGTTTGT | TTCGTTGTTG  |
| 601  | AAGTACGCGG | CCAGCAGCTA | TCTGAGCCTG | ACGCCTGAGC | AGTGGAAAGTC |
|      | TTCATGCGCC | GGTCGTCGAT | AGACTCGGAC | TGCGGACTCG | TCACCTTCAG  |
| 651  | CCACAGAAGC | TACAGCTGCC | AGGTCACGCA | TGAGGGGAGC | ACCGTGGAAG  |
|      | GGTGTCTTCG | ATGTCGACGG | TCCAGTGCGT | ACTCCCCTCG | TGGCACCTTT  |
|      |            | StuI       |            | SphI       |             |
|      |            | ~~~~~      |            | ~~~~~      |             |
| 701  | AAACCGTTGC | GCCGACTGAG | GCCTGATAAG | CATGCGTAGG | AGAAAATATA  |
|      | TTTGGCAACG | CGGCTGACTC | CGGACTATTG | GTACGCATCC | TCTTTTATTT  |
| 751  | ATGAAACAAA | GCACTATTGC | ACTGGCACTC | TTACCGTTGC | TCTTCACCCC  |
|      | TACTTTGTTT | CGTGATAACG | TGACCGTGAG | AATGGCAACG | AGAAGTGGGG  |
|      |            | MfeI       |            |            |             |
|      |            | ~~~~~      |            |            |             |
| 801  | TGTTACCAAA | GCCCAGGTGC | AATTGAAAGA | AAGCGGCCCG | GCCCTGGTGA  |
|      | ACAATGGTTT | CGGGTCCACG | TTAACTTTCT | TTGCGCGGGC | CGGGACCACT  |
|      |            |            |            | BspEI      |             |
|      |            |            |            | ~~~~~      |             |
| 851  | AACCGACCCA | AACCCTGACC | CTGACCTGTA | CCTTTTCCGG | ATTTAGCCTG  |
|      | TTGGCTGGGT | TTGGGACTGG | GACTGGACAT | GGAAAAGGCC | TAAATCGGAC  |
| 901  | TCCACGTCTG | GCGTTGGCGT | GGGCTGGATT | CGCCAGCCGC | CTGGGAAAGC  |
|      | AGGTGCAGAC | CGCAACCGCA | CCCGACCTAA | GCGGTCGGCG | GACCCTTTCG  |
|      |            | XhoI       |            |            |             |
|      |            | ~~~~~      |            |            |             |
|      |            | AvaI       |            |            |             |
|      |            | ~~~~~      |            |            |             |
| 951  | CCTCGAGTGG | CTGGCTCTGA | TTGATTGGGA | TGATGATAAG | TATTATAGCA  |
|      | GGAGCTCACC | GACCGAGACT | AACTAACCTT | ACTACTATTC | ATAATATCGT  |
|      |            |            |            | BstBI      |             |
|      |            |            |            | ~~~~~      |             |
|      |            |            |            | SfuI       |             |
|      |            |            |            | ~~~~~      |             |
|      |            |            |            | NspV       |             |
|      |            |            |            | ~~~~~      |             |
| 1001 | CCAGCCTGAA | AACGCGTCTG | ACCATTAGCA | AAGATACTTC | GAAAAATCAG  |
|      | GGTCGGACTT | TTGCGCAGAC | TGGTAATCGT | TTCTATGAAG | CTTTTATAGT  |
| 1051 | GTGGTGCTGA | CTATGACCAA | CATGGACCCG | GTGGATACGG | CCACCTATTA  |
|      | CACCACGACT | GATACTGGTT | GTACCTGGGC | CACCTATGCC | GGTGGATAAT  |
|      |            | BssHII     |            |            |             |
|      |            | ~~~~~      |            |            |             |
| 1101 | TTGCGCGCGT | TCTCCTCGTT | ATCGTGGTGC | TTTTGATTAT | TGGGGCCAAG  |
|      | AACGCGCGCA | AGAGGAGCAA | TAGCACCACG | AAAATAATA  | ACCCCGGTTC  |

B1pI

Fig. 14 (cont.)

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|      | StyI                     |                           | CelII                    |                          |                           |
|------|--------------------------|---------------------------|--------------------------|--------------------------|---------------------------|
| 1151 | GCACCCTGGT<br>CGTGGGACCA | GACGGTTAGC<br>CTGCCAATCG  | TCAGCGTCGA<br>AGTCGCAGCT | CCAAAGGTCC<br>GGTTTCCAGG | AAGCGTGTTT<br>TTGCGACAAA  |
| 1201 | CCGCTGGCTC<br>GGCGACCGAG | CGAGCAGCAA<br>GCTCGTCGTT  | AAGCACCAGC<br>TTCGTGGTCG | GGCGGCACGG<br>CCGCCGTGCC | CTGCCCTGGG<br>GACGGGACCC  |
| 1251 | CTGCCTGGTT<br>GACGGACCAA | AAAGATTATT<br>TTTCTAATAA  | TCCCGBAACC<br>AGGGCCTTGG | AGTCACCCTG<br>TCAGTGGCAC | AGCTGGAACA<br>TCGACCTTGT  |
| 1301 | GCGGGGCGCT<br>CGCCCCGCGA | GACCAGCGGC<br>CTGGTCGCCG  | GTGCATACCT<br>CACGTATGGA | TTCCGGCGGT<br>AAGGCCGCCA | GCTGCAAAGC<br>CGACGTTTTC  |
| 1351 | AGCGGCCTGT<br>TCGCCGGACA | ATAGCCTGAG<br>TATCGGACTC  | CAGCGTTGTG<br>GTCGCAACAC | ACCGTGCCGA<br>TGGCACGGCT | GCAGCAGCTT<br>CGTCGTCGAA  |
| 1401 | AGGCACTCAG<br>TCCGTGAGTC | ACCTATATTT<br>TGGATATAAA  | GCAACGTGAA<br>CGTTGCACTT | CCATAAACCG<br>GGTATTTGGC | AGCAACACCA<br>TCGTTGTGGT  |
|      |                          |                           |                          | EcoRI                    |                           |
| 1451 | AAGTGGATAA<br>TTCACCTATT | AAAAGTGGAA<br>TTTTACCTTT  | CCGAAAAGCG<br>GGCTTTTTCG | AATTCGGGGG<br>TTAAGCCCCC | AGGGAGCGGG<br>TCCCTCGCCC  |
| 1501 | AGCGGTGATT<br>TCGCCACTAA | TTGATTATGA<br>AACTAATACT  | AAAGATGGCA<br>TTTCTACCGT | AACGCTAATA<br>TTGCGATTAT | AGGGGGCTAT<br>TCCCCCGATA  |
|      |                          |                           |                          | gIIIseq9 100.0%          |                           |
| 1551 | GACCGAAAAT<br>CTGGCTTTTA | GCCGATGAAA<br>CGGCTACTTT  | ACGCGCTACA<br>TGCGCGATGT | GTCTGACGCT<br>CAGACTGCGA | AAAGGCAAAC<br>TTTCCGTTTG  |
|      |                          |                           |                          | Clal                     |                           |
| 1601 | TTGATTCTGT<br>AACTAAGACA | CGCTACTGAT<br>GCGATGACTA  | TACGGTGCTG<br>ATGCCACGAC | CTATCGATGG<br>GATAGCTACC | TTTCATTGGT<br>AAAGTAACCA  |
| 1651 | GACGTTTCCG<br>CTGCAAAGGC | GCCTTGCTAA<br>CGGAACGATT  | TGGTAATGGT<br>ACCATTACCA | GCTACTGGTG<br>CGATGACCAC | ATTTTGCTGG<br>TAAAACGACC  |
| 1701 | CTCTAATTCC<br>GAGATTAAGG | CAAATGGCTC<br>GTTTACCGAG  | AAGTCGGTGA<br>TTCAGCCACT | CGGTGATAAT<br>GCCACTATTA | TCACCTTTAA<br>AGTGGAATTT  |
| 1751 | TGAATAATTT<br>ACTTATTAAA | CCGTCAATAT<br>GGCAGTTATA  | TTACCTTCCC<br>AATGGAAGGG | TCCCTCAATC<br>AGGGAGTTAG | GGTTGAATGT<br>CCAACCTTACA |
| 1801 | CGCCCTTTTG<br>GCGGGAAAAC | TCTTTGGCGC<br>AGAAACCGCG  | TGGTAAACCA<br>ACCATTTGGT | TATGAATTTT<br>ATACTTAAAA | CTATTGATTG<br>GATAACTAAC  |
| 1851 | TGACAAAATA<br>ACTGTTTTAT | AAC TTATTCC<br>TTGAATAAGG | GTGGTGTCTT<br>CACCACAGAA | TGCGTTTCTT<br>ACGCAAAGAA | TTATATGTTG<br>AATATACAAC  |
| 1901 | CCACCTTTAT<br>GGTGGAATA  | GTATGTATTT<br>CATACATAAA  | TCTACGTTTG<br>AGATGCAAAC | CTAACATACT<br>GATTGTATGA | GCGTAATAAG<br>CGCATTATTC  |

Fig. 14 (cont.)

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1951 GAGTCTTGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG  
 CTCAGAATA TTCGAAGTGG ACACCTTCACT TTTTACCGCG TCTAACACGC  
 OGIII3 100.0%  
 =====

2001 ACATTTTTTTT TGTCTGCCGT TTAATGAAAT TGTAAACGTT AATATTTTGT  
 TGTAAAAAAA ACAGACGGCA AATTACTTTA ACATTTGCAA TTATAAAACA

2051 TAAAATTCGC GTTAAATTTT TGTAAATCA GTCATTTTT TAACCAATAG  
 ATTTTAAGCG CAATTTAAAA ACAATTTAGT CGAGTAAAA ATTGGTTATC

2101 GCCGAAATCG GCAAAATCCC TTATAAATCA AAAGAATAGA CCGAGATAGG  
 CGGCTTTAGC CGTTTTAGGG AATATTTAGT TTTCTTATCT GGCTCTATCC

2151 GTTGAGTGTT GTTCCAGTTT GGAACAAGAG TCCACTATTA AAGAACGTGG  
 CAACTCACA CAAGGTCAAA CCTTGTTCTC AGGTGATAAT TTCTTGCAACC

2201 ACTCCAACGT CAAAGGGCGA AAAACCGTCT ATCAGGGCGA TGGCCCACTA  
 TGAGGTTGCA GTTTCCCGCT TTTTGGCAGA TAGTCCCGCT ACCGGGTGAT

2251 CGAGAACCAT CACCCTAATC AAGTTTTTTG GGGTCGAGGT GCCGTAAAGC  
 GCTCTTGGA GTGGGATTAG TTCAAAAAAC CCCAGCTCCA CGGCATTTTCG

2301 ACTAAATCGG AACCCTAAAG GGAGCCCCCG ATTTAGAGCT TGACGGGGAA  
 TGATTTAGCC TTGGGATTTT CCTCGGGGGC TAAATCTCGA ACTGCCCTT

2351 AGCCGGCGAA CGTGGCGAGA AAGGAAGGGA AGAAAGCGAA AGGAGCGGGC  
 TCGGCCGCTT GCACCGCTCT TTCCTTCCCT TCTTTCGCTT TCCTCGCCCG

2401 GCTAGGGCGC TGGCAAGTGT AGCGGTCACG CTGCGCGTAA CCACCACACC  
 CGATCCCGCG ACCGTTTACA TCGCCAGTGC GACGCGCATT GGTGGTGTGG

2451 CGCCGCGCTT AATGCGCCGC TACAGGGCGC GTGCTAGCCA TGTGAGCAAA  
 GCGGCGCGAA TTACGCGGCG ATGTCCCGCG CACGATCGGT ACACCTCGTTT

2501 AGGCCAGCAA AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTTT  
 TCCGGTCGTT TTCCGGTCCT TGGCATTTTT CCGGCGCAAC GACCGCAAAA

2551 TCCATAGGCT CCGCCCCCTT GACGAGCATC AAAAAATCG ACGCTCAAGT  
 AGGTATCCGA GCGGGGGGA CTGCTCGTAG TGTTTTTAGC TGCGAGTTCA

2601 CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC  
 GTCTCCACCG CTTTGGGCTG TCCTGATATT TCTATGGTCC GCAAAGGGGG

2651 TGGAAGCTCC CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT  
 ACCTTCGAGG GAGCACGCGA GAGGACAAGG CTGGGACGGC GAATGGCCTA

2701 ACCTGTCCGC CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA  
 TGGACAGGCG GAAAGAGGGA AGCCCTTCGC ACCGCGAAAG AGTATCGAGT

2751 CGCTGTAGGT ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG  
 GCGACATCCA TAGAGTCAAG CCACATCCAG CAAGCGAGGT TCGACCCGAC

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Fig. 14 (cont.)

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2801 TGTGCACGAA CCCCCCGTTC AGTCCGACCG CTGCGCCTTA TCCGGTAACT  
ACACGTGCTT GGGGGGCAAG TCAGGCTGGC GACGCGGAAT AGGCCATTGA

2851 ATCGTCTTGA GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA  
TAGCAGAACT CAGGTTGGGC CATTCTGTGC TGAATAGCGG TGACCGTCGT

2901 GCCACTGGTA ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA  
CGGTGACCAT TGTCCTAATC GTCTCGCTCC ATACATCCGC CACGATGTCT

2951 GTTCTTGAAG TGGTGGCCTA ACTACGGCTA CACTAGAAGA ACAGTATTTG  
CAAGAACTTC ACCACCGGAT TGATGCCGAT GTGATCTTCT TGTCTATAAC

3001 GTATCTGCGC TCTGCTGTAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC  
CATAGACGCG AGACGACATC GGTCAATGGA AGCCTTTTTC TCAACCATCG

3051 TCTTGATCCG GCAAACAAAC CACCGCTGGT AGCGGTGGTT TTTTGTGTTG  
AGAACTAGGC CGTTTGTTTG GTGGCGACCA TCGCCACCAA AAAACAAAC

3101 CAAGCAGCAG ATTACGCGCA GAAAAAAGG ATCTCAAGAA GATCCTTTGA  
GTTTCGTCGTC TAATGCGCGT CTTTTTTTCC TAGAGTTCTT CTAGGAAACT

3151 TCTTTTCTAC GGGTCTGAC GCTCAGTGGA ACGAAACTC ACGTTAAGGG  
AGAAAAGATG CCCCAGACTG CGAGTCACCT TGCTTTTGAG TGCAATTCCC

3201 ATTTTGGTCA GATCTAGCAC CAGGCGTTTA AGGGCACCAA TAACTGCCTT  
TAAAACCAGT CTAGATCGTG GTCCGCAAAT TCCCGTGGTT ATTGACGGAA

3251 AAAAAAATTA CGCCCCGCCC TGCCACTCAT CGCAGTACTG TTGTAATTCA  
TTTTTTTAAT GCGGGGCGGG ACGGTGAGTA GCGTCATGAC AACATTAAGT

3301 TTAAGCATTC TGCCGACATG GAAGCCATCA CAAACGGCAT GATGAACCTG  
AATTGTAAG ACGGCTGTAC CTTCCGGTAGT GTTTGCCGTA CTACTTGGAC

3351 AATCGCCAGC GGCATCAGCA CCTTGTCGCC TTGCGTATAA TATTTGCCCA  
TTAGCGGTCG CCGTAGTCGT GGAACAGCGG AACGCATATT ATAAACGGGT

3401 TAGTGAAAAC GGGGGCGAAG AAGTTGTCCA TATTGGCTAC GTTTAAATCA  
ATCACTTTTG CCCCCGCTTC TTCAACAGGT ATAACCGATG CAAATTTAGT

3451 AAACCTGGTGA AACTCACCCA GGGATTGGCT GAGACGAAAA ACATATTCTC  
TTTGACCACT TTGAGTGGGT CCCTAACCGA CTCTGCTTTT TGTATAAGAG

3501 AATAAACCTT TTAGGGAAAT AGGCCAGGTT TTCACCGTAA CACGCCACAT  
TTATTTGGGA AATCCCTTTA TCCGGTCCAA AAGTGGCATT GTGCGGTGTA

3551 CTTGCGAATA TATGTGTAGA AACTGCCGGA AATCGTCGTG GTATTCACTC  
GAACGCTTAT ATACACATCT TTGACGGCCT TTAGCAGCAC CATAAGTGAG

+1

3601 CAGAGCGATG AAAACGTTTC AGTTTGCTCA TGGAAAACGG TGTAACAAGG  
GTCTCGCTAC TTTTGCAAAG TCAAACGAGT ACCTTTTGCC ACATTGTTCC

3651 GTGAACACTA TCCCATATCA CCAGCTCACC GTCCTTTCATT GCCATACGGA  
CACTTGTGAT AGGGTATAGT GGTCGAGTGG CAGAAAGTAA CGGTATGCCT

Fig. 14 (cont.)



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3701 ACTCCGGGTG AGCATTTCATC AGGCGGGCAA GAATGTGAAT AAAGGCCGGA  
 TGAGGCCAC TCGTAAGTAG TCCGCCCGTT CTTACACTTA TTTCCGGCCT  
 3751 TAAAACTTGT GCTTATTTTT CTTTACGGTC TTTAAAAGG CCGTAATATC  
 ATTTTGAACA CGAATAAAAA GAAATGCCAG AAATTTTTTC GGCATTATAG  
 3801 CAGCTGAACG GTCTGGTTAT AGGTACATTG AGCAACTGAC TGAAATGCCT  
 GTCGACTTGC CAGACCAATA TCCATGTAAC TCGTTGACTG ACTTTACGGA  
 3851 CAAAATGTTT TTTACGATGC CATTGGGATA TATCAACGGT GGTATATCCA  
 GTTTTACAAG AAATGCTACG GTAACCTAT ATAGTTGCCA CCATATAGGT  
 3901 GTGATTTTTT TCTCCATTTT AGCTTCCTTA GCTCCTGAAA ATCTCGATAA  
 CACTAAAAAA AGAGGTAAAA TCGAAGGAAT CGAGGACTTT TAGAGCTATT  
 3951 CTCAAAAAAT ACGCCCGGTA GTGATCTTAT TTCATTATGG TGAAAGTTGG  
 GAGTTTTTTA TGCGGGCCAT CACTAGAATA AAGTAATACC ACTTTCAACC  
 4001 AACCTCACCC GACGTCTAAT GTGAGTTAGC TCACTCATTG GGCACCCACG  
 TTGGAGTGGG CTGCAGATTA CACTCAATCG AGTGAGTAAT CCGTGGGGTC  
 4051 GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG  
 CGAAATGTGA AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC  
 M13 Reverse primer 100.0%  
 =====  
 4101 ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATT  
 TATTGTTAAA GTGTGTCCTT TGTCGATACT GGTACTAATG CTAA

Fig. 14 (cont.)